



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12Q 1/68, A62D 3/00	A2	(11) International Publication Number: WO 00/63443 (43) International Publication Date: 26 October 2000 (26.10.00)
(21) International Application Number: PCT/US00/09883 (22) International Filing Date: 13 April 2000 (13.04.00) (30) Priority Data: 60/129,511 15 April 1999 (15.04.99) US (71) Applicant (for all designated States except US): E.I. DU PONT DE NEMOURS AND COMPANY [US/US]; 1007 Market Street, Wilmington, DE 19898 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): HENDRICKSON, Edwin, R. [US/US]; 49 Kings Grant Road, Hockessin, DE 19707 (US). EBERSOLE, Richard, C. [US/US]; 2412 Dacia Drive, Wilmington, DE 19810 (US). (74) Agent: FELTHAM, S., Neil; E.I. du Pont de Nemours and Company, Legal Patent Records Center, 1007 Market Street, Wilmington, DE 19898 (US).		(81) Designated States: CA, MX, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING BACTERIA (57) Abstract A unique 16S rRNA profile derived from <i>Dehalococcoides ethenogenes</i> has been identified and isolated. The profile contains a nucleic acid fragment that is linked to dechlorinating activity. This sequence is set forth in SEQ ID NO:1.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

TITLENUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION
OF DECHLORINATING BACTERIAFIELD OF THE INVENTION

5 The invention relates to the field of molecular biology and microbiology. More specifically, 16S rRNA regions of been identified and isolated from *Dehalococcoides ethenogenes* that enable the identification of dechlorinating bacterial strains. Probes and primers corresponding to the unique regions have been constructed to enable the rapid identification of the dechlorinators.

10

BACKGROUND

Groundwater pollution by halogenated, and particularly chlorinated solvents is a worldwide problem associated primarily with industrial sites where mishandling or improper disposal has brought these solvents in contact with the soil. The most common and problematic compounds are the chlorinated ethylenes (ethenes) such as tetra- tri- or di-chloroethylene. Carbon tetrachloride, chloroform and methylene chloride are also pervasive pollutants. The reasons for concern are basically threefold. First, most of these solvents are sparingly soluble in water and have the tendency to stick to soil particles. This results in tenacious underground plumes of solvent which cannot readily be removed by standard pump and treat technology (Biswas, N., et al., *Water Environ. Res.* 64, 170, 10, 1 (1992); Hutter, G. M., et. al., *Water Environ. Res.* 64, 69, (1992)). Second, the toxicology of many chlorinated solvents suggests that these compounds may be carcinogenic and damaging to specific organs such as the liver and kidneys (Price, P. S., Memo of the U.S. Environmental Protection Agency, Office of Water, Washington, D.C.(1985); Vogel, T. M., *Environ. Sci. Technol.*, 21, 722, (1987)). Finally, under conditions found in many aquifers and subsurface environments, chlorinated ethylenes and methanes are very slow to be degraded biologically. The result of these factors is that chlorinated solvents are long-lived potentially hazardous groundwater pollutants.

30 Currently there are two approaches to in situ removal of organohalogen pollutants. The first approach is the standard "pump and treat" method where groundwater is pumped to the surface for physical stripping of the contaminant from the water. For chlorinated solvents this is more of a containment method than a remediation technology although given sufficient time (typically decades to centuries) this method may capture most of the pollutant. The other approach is biological in nature and utilizes microorganisms for the enzymatic transformation of the halogenated organics. The biological approach may utilize microorganisms indigenous to a particular site where the remediation process consists primarily of

making additions to the contaminated site that enhance the growth of the desired microorganism. Alternatively, nonindigenous microorganisms may be introduced to a contaminated site with the necessary amendments needed for growth.

5 A number of organisms are known to dechlorinate persistent chlorinated pollutants. For example, *Dehalobacter restrictus* and *Dehalospirillum*
multivorans, have been shown to partially dechlorinate chlorinated ethenes (Kochian et al., *Plant Mol. Biol.* 46:237 (1995); Delhaize et al., *Plant Physiol.* 107:315 (1995)). Similarly, *Dehalococcoides ethenogenes* has been shown to effect the complete dechlorination of tetrachloroethene and trichloroethene to
10 ethene [Freedman et al., *Appl. Environ. Microbiol.* 55:2144 (1989)] and Maymó-Gatell et al. (*Science*, 176:1568 (1997)) have isolated a *D. ethenogenes* strain that is capable of respiratory reductive dechlorination of tetrachloroethene directly to ethene with hydrogen as an electron donor. Analysis of the 16S rRNA of the Maymó-Gatell organism revealed a unique profile that may be used to
15 identify organisms of similar reductive capabilities.

The first step in utilizing the dechlorinating properties of the above identified organisms is rapid and accurate identification. One method of identification involves the use of DNA probes (see for example in WO 89/06704, U.S. Patent No. 4,851,330, and U.S. Patent No. 5,574,145). Many such probes
20 derive from the observation (see Woese, *Scientific American* 244 (6) 1981 for review) that parts of the 16S and 23s ribosomal RNA (rRNA) sequences vary in different species. This information was used initially for phylogenetic analyses but it has more recently been used for DNA probe-based methods for the identification of organisms. The utility of such a method is based on the
25 conservation of nucleic acid sequence within the rRNA sequences.

Each of the cells of all life forms, except viruses, contain ribosomes and therefore ribosomal RNA. A ribosome contains three separate single strand RNA molecules, namely, a large molecule, a medium sized molecule, and a small molecule. The two larger rRNA molecules vary in size in different organisms.
30 Ribosomal RNA is a direct gene product and is coded for by the rRNA gene. This DNA sequence is used as a template to synthesize rRNA molecules. A separate gene exists for each of the ribosomal RNA subunits. Multiple rRNA genes exist in most organisms, many higher organisms containing both nuclear and mitochondrial rRNA genes. Numerous ribosomes are present in all cells of all life
35 forms. About 85-90 percent of the total RNA in a typical cell is rRNA. A bacteria such as *E. coli* contains about 10^4 ribosomes per cell. Much of the sequences in rRNA highly conserved across broad evolutionary boundaries,

however, certain regions are highly variable and may be used to make fine distinctions between species, sub-species and strains (U.S. Patent No. 5567587).

The problem to be overcome therefore is to identify a unique 16S rDNA sequence in a bacteria capable of dechlorination of persistent chlorinated compounds for the identification and ultimate enhancement of that bacteria to remediate a contaminated site. Applicants have solved the state problem by providing a set of nucleic acid sequences that are unique to various strains of *Dehalococcoides ethenogenes*.

SUMMARY OF THE INVENTION

The present invention provides an isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain selected from the group consisting of: (a) SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:30; (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS at 65 °C; and (c) an isolated nucleic acid molecule that is completely complementary to (a) or (b).

The invention further provides primers useful for the identification of new dechlorinating bacteria selected from the group consisting of: SEQ ID NOs:9-29; and any sequences that hybridize under conditions of 0.1X SSC, 0.1% SDS at 65 °C to those primers.

The invention additionally provides an isolated bacterial strain comprising any one of the sequences of the instant invention as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:30, wherein said strain has the ability to dechlorinate chlorinated compounds.

The invention further provides a method for identifying a dechlorinating bacterial strain comprising: (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds; (ii) probing the extracted genomic DNA with a probe derived from any one of the sequences instant invention as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:30, under suitable hybridization conditions, wherein the identification of a hybridizable nucleic acid fragment

confirms the presence of a bacteria capable of dechlorinating chlorinated compounds.

Similarly the invention provides a method for identifying a dechlorinating bacterial strain comprising (i) extracting genomic DNA from a cell suspected of
5 being able to dechlorinate chlorinated compounds; and (ii) amplifying the extracted genomic DNA with an oligonucleotide primer corresponding to a portion of any one of the sequences instant invention as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ
10 ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:30, such that amplification products are generated wherein the presence of amplification products confirms the presence of a dechlorinating bacterial strain.

The invention additionally provides a method for the dechlorination of
15 chlorinated compounds comprising contacting a chlorinated compound with an isolated bacterial strain comprising any one of the DNA fragments as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID
20 NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:30 under conditions suitable for dechlorination to occur.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE LISTING

Figure 1 is an alignment of 16S rDNA sequence profile from
25 *Dehalococcoides ethenogenes* DHE-195 as disclosed in Maymó-Gatell et al., *Science*, 176:1568 (1997), as compared with profiles generated for organisms isolated from a number of wastewater treatment sites.

Figure 2 is a comparison of the instant dechlorinating 16S rDNA profiles with a 16S rDNA profile from *E. coli*.

30 Figure 3 is a graph illustrating the ability of a soil microcosm or culture developed from certain soils taken from a chloroethene contaminated site to dechlorinate trichloroethylene or perchloroethylene.

Figure 4 is an image of an electrophoresis gel used to detect PCR products in a test of soils contaminated with chloroethenes using two sets of the primers
35 described herein.

The following sequence descriptions and sequences listings attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825. The

Sequence Descriptions contain the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IYUB standards described in *Nucleic Acids Research* 13:3021-3030 (1985) and in the *Biochemical Journal* 219 (No. 2):345-373 (1984) which are
5 herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

SEQ ID NO:1 is a unique region of the *Dehalococcoides ethenogenes* 16S rDNA profile which is linked to dechlorinating activity.

10 SEQ ID NO:2 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-PL, isolated from soil surrounding in industrial site.

SEQ ID NO:3 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-STF, isolated from soil surrounding in industrial site.

SEQ ID NO:4 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-DAB, isolated from soil surrounding in industrial site.

15 SEQ ID NO:5 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-PIN, isolated from soil surrounding in industrial site.

SEQ ID NO:6 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-DLL, isolated from soil surrounding in industrial site.

20 SEQ ID NO:7 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-195 as reported in Maymó-Gatell et al. (*Science*, 176:1568 (1997)), Genbank AF004928.

SEQ ID NO:8 is the consensus sequence derived from DHE-PL, DHE-STF, DHE-DAB, DHE-PIN, and DHE-DLL at bases E180-E226.

25 SEQ ID NO:9-29 are primers derived from the 16S rDNA profile, useful in the identification of dechlorinating bacteria.

SEQ ID NO:30 is the consensus sequence derived from DHE-PL, DHE-STF, DHE-DAB, DHE-PIN, and DHE-DLL at bases E1001-E1047.

SEQ ID NO:31 is the base sequence in the region of the consensus 16S rDNA profile from where the diagnostic sequence is derived.

30 SEQ ID NO:32 is the base sequence in the region of the DHE-195 16S rDNA profile from where the diagnostic sequence is derived.

SEQ ID NO:33 is the *E. coli* reference 16S rDNA sequence.

DETAILED DESCRIPTION OF THE INVENTION

35 The present invention provides unique 16S rDNA sequence profiles derived from *Dehalococcoides ethenogenes* (DHE). *D. ethenogenes* is known for its ability to degrade persistent chlorinated pollutants. The instant sequence profiles may be used to identify and sub-type bacteria with similar metabolic pathways. One sequence (ATTTCTAGCGAGACTGCCCCGCG, SEQ ID

NO:1), beginning at base E1146, has been identified in all DHE's isolated from contaminated soils and is strongly linked to the ability of these organisms to degrade chlorinated organics. Similarly, a stretch of nucleic acids ranging between E180 and E226, corresponding to SEQ ID NO:8 may be used to identify
5 dechlorinators as well as for genetic sub-typing of species.

In this disclosure, a number of terms and abbreviations are used. The following definitions are provided.

The term "*Dehalococcoides ethenogenes*" will be abbreviated "DHE".

The term "DHE-195" will refer to the strains of *Dehalococcoides*
10 *ethenogenes* isolated and characterized by Maymó-Gatell et al. (*Science*, 176:1568 (1997)).

The terms "DHE-PL, DHE-STF, DHE-DAB, DHE-DLL and DHE-PIN" will refer to strains of *Dehalococcoides sp.* containing the instant dechlorinating 16S rDNA profile.

15 The term "dechlorinating bacteria" refers to any bacterial species or strain that has the ability to remove at least one chlorine atom from a chlorinated organic compound. Dechlorinating bacteria may have the ability to grow on chlorinated organics as a sole carbon source, or may prefer degradation using an alternate energy source.

20 The term "chlorinated compounds" will mean any straight chain or ring containing organic compound which contains at least one chlorine atom.

Trichloroethylene will be abbreviated "TCE".

Perchloroethylene will be abbreviated "PCE".

25 The term "16S rDNA" will refer to the DNA encoding ribosomal RNA found within bacterial cells.

The term "16S rDNA profile" will refer to the specific DNA sequence of the rDNA gene in any particular organism. For the purposes of the present invention the 16S rDNA profiles for DHE-195, DHE-PL, DHE-STF, DHE-DAB, DHE-DLL and DHE-PIN are illustrated in Figures 1 and 2.

30 The term "signature sequence" or signature sequence region" will refer to those short sequences in the 16S gene or rRNA molecule which are unique to a certain group or groups of organisms. These sequences can be used to define domains, group, subdivisions genera or species of an organism.

35 The term "consensus sequence" as used herein, as it relates to the alignment of a given set of sequences, will be defined as the sequence of the set of bases where a designated base is the one that occurs most often at each position in the 16S sequence.

The term "reference sequence" as used herein, as it relates to the alignment of a given set of sequences, will be defined as the particular 16S sequence to which the bases at each position of an alignment of 16S sequences are compared. The reference sequence used herein was an *E. coli* 16S rDNA sequence. Bases identified in the reference sequence that correlate to corresponding bases in a 16S rDNA profile are assigned an "E number". Thus, the base labeled E-27 on the reference sequence corresponds to base 1 of the 16S rDNA profile of DHE-195 and E-107 corresponds to base 66 of DHE-195. The complete correlation is given in Table 2.

10 The term "dechlorinating 16S rDNA profile" will refer to a 16S rDNA profile containing the diagnostic sequence as set forth in SEQ ID NO:1.

The term "diagnostic sequence" will refer to the sequence ATTTTCTAGCGAGACTGCCCCGCG (SEQ ID NO:1) which is indicative of dechlorinating activity.

15 The letters "A", "G", "T", "C" when referred to in the context of nucleic acids will mean the purine bases Adenine (C₅H₅N₅), Guanine (C₅H₅N₅O) and the pyrimidine bases Thymine (C₅H₆N₂O₂) and Cytosine (C₄H₅N₃O) respectively.

20 In this disclosure, a number of terms and abbreviations are used. The following definitions are provided.

"Gene" refers to a nucleic acid fragment that expresses a specific protein, including regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence.

25 The term "nucleic acid fragment" will refer to a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

30 The term "oligonucleotide" refers to primers, probes, oligomer fragments to be detected, labeled-replication blocking probes, oligomer controls, and shall be generic to polydeoxyribonucleotides (containing 2-deoxy-D-ribose), to polyribonucleotides (containing D-ribose) and to any polynucleotide which is an N glycoside of a purine or pyrimidine base (nucleotide), or modified purine or pyrimidine base. Also included in the definition of "oligonucleotide" are nucleic acid analogs (e.g., peptide nucleic acids) and those that have been structurally modified (e.g., phosphorothioate linkages). There is no intended distinction between the length of a "nucleic acid", "polynucleotide" or an "oligonucleotide".

35 The term "primer" refers to an oligonucleotide (synthetic or occurring naturally), which is capable of acting as a point of initiation of nucleic acid

synthesis or replication along a complementary strand when placed under conditions in which synthesis of a complementary strand is catalyzed by a polymerase.

5 The term "probe" refers to an oligonucleotide (synthetic or occurring naturally), that is significantly complementary to a "fragment" and forms a duplexed structure by hybridization with at least one strand of the fragment.

The term "complementary" is used to describe the relationship between nucleotide bases that are hybridizable to one another. For example, with respect to DNA, adenosine is complementary to thymine and cytosine is complementary
10 to guanine.

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength.
15 Hybridization and washing conditions are well known and exemplified in Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor (1989), particularly Chapter 11 and Table 11.1 therein (entirely incorporated herein by reference). The conditions of temperature and ionic
20 strength determine the "stringency" of the hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of 55°, can be used, e.g., 5X SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5X SSC, 0.5% SDS. Moderate stringency hybridization conditions correspond to a higher T_m , e.g., 40% formamide, with
25 5X or 6X SSC.

Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of
30 complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater
35 than 100 nucleotides in length, equations for calculating T_m have been derived (see Sambrook et al., *supra*, 9.50-9.51, hereby incorporated by reference). For hybridizations with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide

determines its specificity (see Sambrook et al., *supra*, 11.7-11.8, hereby incorporated by reference). In one embodiment the length for a hybridizable nucleic acid is at least about 10 nucleotides. Preferable a minimum length for a hybridizable nucleic acid is at least about 15 contiguous nucleotides; more preferably at least about 20 contiguous nucleotides; and most preferably the length is at least 30 contiguous nucleotides. Thus, where a "probe" or "primer" is "derived from" or corresponds to a "portion" of a nucleic acid fragment, the probe or primer or portion will preferably be at least about 15 contiguous nucleotides; more preferably at least about 20 contiguous nucleotides; and most preferably the length is at least 30 contiguous nucleotides of the fragment from which it is derived. Furthermore, the skilled artisan will recognize that the temperature and wash solution salt concentration may be adjusted as necessary according to factors such as length of the probe.

The term "amplification product" refers to portions of nucleic acid fragments that are produced during a primer directed amplification reaction. Typical methods of primer directed amplification include polymerase chain reaction (PCR), ligase chain reaction (LCR) or Strand displacement Amplification (SDA). If PCR methodology is selected, the replication composition would include for example, nucleotide triphosphates, two primers with appropriate sequences, DNA or RNA polymerase and proteins. These reagents and details describing procedures for their use in amplifying nucleic acids are provided in U.S. Patent No. 4,683,202 (1987, Mullis, et al.) and U.S. Patent No. 4,683,195 (1986, Mullis, et al.). If LCR methodology is selected, then the nucleic acid replication compositions would comprise, for example, a thermostable ligase, e.g., *T. aquaticus* ligase, two sets of adjacent oligonucleotides wherein one member of each set is complementary to each of the target strands, Tris HCl buffer, KCl, EDTA, NAD, dithiothreitol and salmon sperm DNA. See, for example, Tabor et al., *Proc. Acad. Sci. U.S.A.*, 82, 1074-1078 (1985)).

The term "sequence analysis software" refers to any computer algorithm or software program that is useful for the analysis of nucleotide or amino acid sequences. "Sequence analysis software" may be commercially available or independently developed. Typical sequence analysis software will include but is not limited to the GCG suite of programs (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, Wisc.), BLASTP, BLASTN, BLASTX (Altschul et al., *J. Mol. Biol.* 215:403-410 (1990), and DNASTAR (DNASTAR, Inc., 1228 S. Park St. Madison, WI 53715 USA). Within the context of this application it will be understood that where sequence analysis software is used for analysis, that the results of the analysis will be based on the

“default values” of the program referenced, unless otherwise specified. As used herein “default vales” will mean any set of values or parameters which originally load with the software when first initialized.

Standard recombinant DNA and molecular cloning techniques used here
5 are well known in the art and are described by Sambrook, J., Fritsch, E. F. and Maniatis, T., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (hereinafter “Maniatis”); and by Silhavy, T. J., Bennis, M. L. and Enquist, L. W.,
Experiments with Gene Fusions, Cold Spring Harbor Laboratory Cold Press
10 Spring Harbor, NY (1984); and by Ausubel, F. M. et al., Current Protocols in Molecular Biology, published by Greene Publishing Assoc. and Wiley-Interscience (1987).

The present invention relates to unique 16S rDNA sequences which have been isolated from the bacteria very similar if not related to *Dehalococcoides*
15 *ethenogenes*, which are associated with the ability of this bacteria to dechlorinate chlorinated organic compounds. The sequences were isolated from bacteria found in soil samples of various industrial sites that have been shown to contain bacteria that have the ability to dechlorinate chlorinated compounds. The sequences are useful for the identification new dechlorinating bacteria, as well as for sub-typing
20 strains of *Dehalococcoides ethenogenes*.

Dechlorinating bacteria were isolated from the aquifer soil taken from around industrial sites by means well known in the art. Samples were maintained under anaerobic conditions and cultured in a suitable medium for the growth of anaerobic soil bacteria. Such culture procedures and media are common and well
25 known in the art and are described in Manual of Methods for General Bacteriology (Phillipp Gerhardt, R. G. E. Murray, Ralph N. Costilow, Eugene W. Nester, Willis A. Wood, Noel R. Krieg and G. Briggs Phillips, eds), American Society for Microbiology, Washington, DC. (1994)) or by Thomas D. Brock in Biotechnology: A Textbook of Industrial Microbiology, Second Edition, Sinauer
30 Associates, Inc., Sunderland, MA (1989).

In order to enrich the cultured soil samples for dechlorinating bacteria, the samples were contacted with a low level of chlorinated organic compound. A number of chlorinated compounds are suitable for this purpose, including, but not limited to carbontetrachloride, tetrachloroethene, chloroform, dichloromethane,
35 trichloroethene, dichloroethylene, vinyl chloride, and chloroaromatics, where chlorinated ethenes are preferred and TCE and PCE are preferred. Incubation proceeded for about six months, and cultures were analyzed periodically for the disappearance of the chlorinated organic and the appearance of degradation

products. Cultures demonstrating the ability to degrade chlorinated organics, were selected for further analysis.

Bacteria from dechlorinating cultures were removed by standard methods and total chromosomal DNA was isolated from the microorganisms through a bead mill homogenization procedure. A fragment of the 16S rRNA gene was amplified from the genomic DNA extract by PCR using 16S rDNA primers specific for dechlorinating microbes. The 16S rDNA PCR product was cloned and sequenced to confirm its identity (M. I. More et al. 1994. *Appl. Environ. Microbiol.*, 60, 1572-1580). Each raw 16S sequences obtained were assembled into a contig, and a consensus was manually constructed using Seqman II in DNASTar (DNASTar, Inc., Madison, WI). For each test sequence, a Pearson and Lipman similarity search was performed using the FASTA program in GCG (Wisconsin Package Version 9.0, Genetics Computer Group, Madison, WI). The nearest organism in similarity in 16S rRNA sequence to the test sequence was used as the nearest match for identification. Those 16S DNA gene sequences that were identified to be similar to the dechlorinating bacteria, *Dehalococcoides ethenogenes* DHE-195 (GenBank Accession No. AF004928), were aligned with selected 16S rRNA sequences extracted from the Ribosomal Database Project (Michigan State University) that were a representation of the major microorganism domains, Bacteria and Archeae in the Universal Phylogenetic Tree of Life. The sequences were aligned using MegAlign in DNASTar, using the default software parameters. From this alignment probable region for signature sequences were mapped. Then sequences from each region were tested against the Ribosomal Database (RDB) for unique sequences that could be signature sequences and utilized as PCR primes or detection probes.

Within the 16S rDNA profile defined by the comparison of the isolated dechlorinators, (see Figures 1 and 2) three signature regions showed considerable variation from the known sequences. Those regions were defined as extending from E1146 to E1156 (SEQ ID NO:1), from E180 to E227 (SEQ ID NO:8), and from E1001 to E1047 (SEQ ID NO: 30). All of the dechlorinating isolates of the present invention contained the sequence as set forth in SEQ ID NO:1, which is conspicuously absent from the sequence known in the art (Maymó-Gatell et al. (*Science*, 176:1568 (1997))).

Although a region similar to that defined by SEQ ID NO:8 is found in the literature sequence, there are significant variations at positions, E184, E190, E197, E200, E207, E216, and E221 as shown below in Formula I.

Formula I.

E184	E190	E198	E201	E208	E217	E222

5 TGTGRTGGGCY GACATAWGTY GGTTCAYTAA AGCCGYAAGGYGC TTG (SEQ ID NO:8)

With in the context the present invention Applicants have discovered that within the signature region defined by SEQ ID NO:8 and Formula I above, the R at position E184 may be A/G, the Y at position E190 may be C/T, the W at position E198 may be A/T, and the Y's at position E201, E208, E217, and E222 may be T/C.

Similarly the region defined by SEQ ID NO:30 is also found in the literature but contains significant variations at positions, E1003, E1012, E1020, E1039, and E1040 as shown below in Formula II.

15 Formula II.

E1003	E1012	E1020	E1039

20 TGWAGTAGTGAACMGAAAGGGRAACGACCTGTTAAGTCAGGARMTTGCACA (SEQ ID NO:30)

E1040

As with SEQ ID NO:8, Applicants have discovered that within the signature region defined by SEQ ID NO:30 and Formula II above, the W at position E1003 may be A/T, at position E1012 the M may be A/C, at position E1020 the R may be A/G, at position E1039 the R may be A/G and , at position E1040 the M may be A/C.

Likewise, if the entire 16S rDNA profile is examined, it is seen that there are significant single base differences throughout the entire profile (Figures 1 and 2). These differences are illustrated in tabular form in Table 2. Accordingly a 16S rDNA profile sequence, having the following bases substitutions taken independently or together will be diagnostic for dechlorinating bacteria: E107=G, base E184=G, base E190=C, E 198=T, E201= T, E208=C, E217=T, E222=C, E264=C, E267=C, E291=T, E333= C, E420=C, E444=T, E631=A, E829=A, E933=T, E934=T, E980=C, E1003=T, E1012=T, E1020=G, E1039=A, E1040=C, E1087=T, and E1114=C.

Assay Methods

The instant sequences may be used in a variety of formats for the detection of dechlorinating bacteria. The two most convenient formats will rely on methods

of nucleic acid hybridization or primer directed amplification methods such as PCR.

Nucleic Acid Hybridization Methods

5 The basic components of a nucleic acid hybridization test include a probe, a sample suspected of containing a dechlorinating bacteria and a specific hybridization method. As noted above, probes of the present invention are single strand nucleic acid sequence which is complementary to the nucleic acid sequences to be detected. Probes are "hybridizable" to the nucleic acid sequence to be detected. The probe length can vary from 5 bases to tens of thousands of bases, and will depend upon the specific test to be done. Only part of the probe molecule need be complementary to the nucleic acid sequence to be detected. In addition, the complementarity between the probe and the target sequence need not be perfect. Hybridization does occur between imperfectly complementary molecules with the result that a certain fraction of the bases in the hybridized region are not paired with the proper complementary base. A probe may be composed of either RNA or DNA. The form of the nucleic acid probe may be a marked single strand molecule of just one polarity or marked single strand molecule having both polarities present. The form of the probe, like its length, will be determined by the type of hybridization test to be done.

20 The sample may or may not contain the organism of interest. The sample may take a variety of forms, including liquid such as water, or solid such as dust, or soil. The sample nucleic acid must be made available to contact the probe before any hybridization of probe and target molecule can occur. Thus the organism's RNA must be free from the cell and placed under the proper conditions before hybridization can occur. Methods of in solution hybridization necessitate the purification of the RNA in order to be able to obtain hybridization of the sample rRNA with the probe. This has meant that to utilize the in solution method for detecting target sequences in a sample, the nucleic acids of the sample must first be purified to eliminate protein, lipids, and other cell components, and then contacted with the probe under hybridization conditions. Method for the purification of the sample nucleic acid are common and well known in the art (Maniatis, *supra*).

35 Similarly, hybridization methods are well defined. Typically the probe and sample must be mixed under conditions which will permit nucleic acid hybridization. This involves contacting the probe and sample in the presence of an inorganic or organic salt under the proper concentration and temperature conditions. The probe and sample nucleic acids must be in contact for a long enough time that any possible hybridization between the probe and sample nucleic

acid may occur. The concentration of probe or target in the mixture will determine the time necessary for hybridization to occur. The higher the probe or target concentration the shorter the hybridization incubation time needed.

In one embodiment, hybridization assays may be conducted directly on bacterial lysates, without the need to extract the nucleic acids. This eliminates several steps from the sample-handling process and speeds up the assay. To perform such assays on crude cell lysates, a chaotropic agent is typically added to the cell lysates prepared as described above. The chaotropic agent stabilizes nucleic acids by inhibiting nuclease activity. Furthermore, the chaotropic agent allows sensitive and stringent hybridization of short oligonucleotide probes to RNA at room temperature [Van Ness and Chen (1991) *Nucl. Acids Res.* 19:5143-5151]. Suitable chaotropic agents include guanidinium chloride, guanidinium thiocyanate, sodium thiocyanate, lithium tetrachloroacetate, sodium perchlorate, rubidium tetrachloroacetate, potassium iodide, and cesium trifluoroacetate, among others. Typically, the chaotropic agent will be present at a final concentration of about 3M. If desired, one can add formamide to the hybridization mixture, typically 30-50% (v/v).

Alternatively, one can purify the rRNA prior to probe hybridization. A variety of methods are known to one of skill in the art (e.g., phenol-chloroform extraction, IsoQuick extraction (MicroProbe Corp., Bothell, WA), and others). Pre-hybridization purification is particularly useful for standard filter hybridization assays. Furthermore, purification facilitates measures to increase the assay sensitivity by incorporating *in vitro* RNA amplification methods such as self-sustained sequence replication (see for example Fahy et al. (1991) in PCR Methods and Applications, Cold Spring Harbor Laboratory Press, pp. 25-33) or reverse transcriptase PCR (Kawasaki (1990) in PCR Protocols: A Guide to Methods and Applications, M. A. Innis et al., eds., pp. 21-27). One can obtain amplified rRNA by using *in vitro* RNA amplification techniques as described in Fahy et al., *supra.*; Kawasaki, *supra.* The exact procedure used is not crucial, provided that it does not amplify significant amounts of DNA, which would tend to obscure results.

Once the pre-rRNA is released from the cells, it can be detected by any of a variety of methods. The method of rRNA detection is not crucial to the invention. However, the most useful embodiments have at least some of characteristics of speed, convenience, sensitivity, and specificity. Direct DNA probe analysis is suitable, as is an *in vitro* RNA amplification method, such as 3SR, that employs labelled primers.

Various hybridization solutions can be employed. Typically, these comprise from about 20 to 60% volume, preferably 30%, of a polar organic solvent. A common hybridization solution employs about 30-50% v/v formamide, about 0.15 to 1M sodium chloride, about 0.05 to 0.1M buffers, such as sodium citrate, Tris-HCl, PIPES or HEPES (pH range about 6-9), about 0.05 to 0.2% detergent, such as sodium dodecylsulfate, or between 0.5-20 mM EDTA, FICOLL (Pharmacia Inc.) (about 300-500 kilodaltons), polyvinylpyrrolidone (about 250-500 kdal), and serum albumin. Also included in the typical hybridization solution will be unlabeled carrier nucleic acids from about 0.1 to 5 mg/mL, fragmented nucleic DNA, e.g., calf thymus or salmon sperm DNA, or yeast RNA, and optionally from about 0.5 to 2% wt./vol. glycine. Other additives may also be included, such as volume exclusion agents which include a variety of polar water-soluble or swellable agents, such as polyethylene glycol, anionic polymers such as polyacrylate or polymethylacrylate, and anionic saccharidic polymers, such as dextran sulfate.

Nucleic acid hybridization is adaptable to a variety of assay formats. One of the most suitable is the sandwich assay format. The sandwich assay is particularly adaptable to hybridization under non-denaturing conditions. A primary component of a sandwich-type assay is a solid support. The solid support has adsorbed to it or covalently coupled to it immobilized nucleic acid probe that is unlabeled and complementary to one portion of the rRNA sequence. Preferred are those probes that hybridize to regions of the rRNA that have minimal secondary and tertiary interactions. The advantage of such probes is that the hybridization can be carried out without the additional step of heat denaturing the sample nucleic acid. For example, the hybridization can be carried out at room temperature.

The sandwich assay may be encompassed in an assay kit. This kit would include a first component for the collection of samples from soil such as vials for containment, and buffers for the disbursement and lysis of the sample. A second component would include media in either dry or liquid form for the hybridization of target and probe polynucleotides, as well as for the removal of undesirable and nonduplexed forms by washing. A third component includes a solid support (dipstick) upon which is fixed or to which is conjugated unlabeled nucleic acid probe(s) that is(are) complementary to a part of the precursor rRNA of the species of bacteria being tested. In the case of multiple target analysis more than one capture probe, each specific for its own rRNA, will be applied to different discrete regions of the dipstick. A fourth component would contain labeled probe that is complementary to a second and different region of the same rRNA strand to

which the immobilized, unlabeled nucleic acid probe of the third component is hybridized.

In another embodiment, the instant 16S rDNA sequence may be used as a 3' blocked detection probe in either a homogeneous or heterogeneous assay format. For example a probe generated from the instant sequences may be 3' blocked or non-participatory and will not be extended by, or participate in, a nucleic acid amplification reaction. Additionally, the probe incorporates a label that can serve as a reactive ligand that acts as a point of attachment for the immobilization of the probe/analyte hybrid or as a reporter to produce detectable signal. Accordingly, genomic or cDNA isolated from the test organism is amplified by standard primer-directed amplification protocols in the presence of an excess of the 16S rDNA 3' blocked detection probe to produce amplification products. Because the probe is 3' blocked, it does not participate or interfere with the amplification of the target. After the final amplification cycle, the detection probe anneals to the relevant portion of the amplified DNA and the annealed complex is then captured on a support through the reactive ligand.

PCR Assay Methods

In an alternate embodiment the present sequences may be used as primers or to generate primers that may be used in primer directed nucleic acid amplification to detect the presence of dechlorinating bacteria. A variety of primer directed nucleic acid amplification methods are known in the art including thermal cycling methods such as polymerase chain reaction (PCR) and ligase chain reaction (LCR) as well as isothermal methods and strand displacement amplification (SDA). The preferred method is PCR. Typically, in PCR-type amplification techniques, the primers have different sequences and are not complementary to each other. Depending on the desired test conditions, the sequences of the primers should be designed to provide for both efficient and faithful replication of the target nucleic acid. Methods of PCR primer design are common and well known in the art. (Thein and Wallace, "The use of oligonucleotide as specific hybridization probes in the Diagnosis of Genetic Disorders", in *Human Genetic Diseases: A Practical Approach*, K. E. Davis Ed., (1986) pp. 33-50 IRL Press, Herndon, Virginia); Rychlik, W. (1993) In White, B. A. (ed.), Methods in Molecular Biology, Vol. 15, pages 31-39, PCR Protocols: Current Methods and Applications. Humana Press, Inc., Totowa, NJ.)

If a nucleic acid target is to be exponentially amplified, then two primers are used each having regions complementary to only one of the stands in the target. After heat denaturation, the single-stranded target fragments bind to the respective primers which are present in excess. Both primers contain asymmetric

restriction enzyme recognition sequences located 5' to the target binding sequences. Each primer-target complex cycles through nicking and polymerization/displacement steps in the presence of a restriction enzyme, a DNA polymerase and the three dNTP's and one dNTP[aS] as discussed above. An in
5 depth discussion of SDA methodology is given by Walker et al., *Proc. Natl. Acad. Sci. U.S.A.*, 89, 392, (1992).

Alternatively, asymmetric amplification can be used to generate the strand complementary to the detection probe. Asymmetric PCR conditions for
10 producing single-stranded DNA would include similar conditions for PCR as described however, the primer concentrations are changed with 50 pmol of the excess primer and 1 pmol of the limiting primer. It is contemplated that this procedure would increase the sensitivity of the method. This improvement in sensitivity would occur by increasing the number of available single strands for binding with the detection probe.

15 Within the context of the present invention primers will be designed to conserved regions of the 16S rDNA profile which are associated with dechlorination. The most significant of those regions are the sequences set forth in SEQ ID NO:1, SEQ ID NO:8 and SEQ ID NO:30.

Following amplification and prior to sequencing, the amplified nucleotide
20 sequence may be ligated to a suitable vector followed by transformation of a suitable host organism with said vector. One thereby ensures a more readily available supply of the amplified sequence. Alternatively, following amplification, the amplified sequence or a portion thereof may be chemically synthesized for use as a nucleotide probe. In either situation the DNA sequence of
25 the variable region is established using methods such as the dideoxy method (Sanger, F. et al. *Proc. Natl. Acad. Sci* (1977) 74, 5463-5467). The sequence obtained is used to guide the choice of the probe for the organism and the most appropriate sequence(s) is/are selected.

EXAMPLES

30 The present invention is further defined in the following Examples. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit
35 and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions.

GENERAL METHODS

Standard recombinant DNA and molecular techniques used in the Examples are well known in the art. Techniques suitable for use in the following examples may be found in Sambrook, J., Fritsch, E. F. and Maniatis, T.,

5. Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (hereinafter "Maniatis").

- Materials and methods suitable for the maintenance and growth of bacterial cultures are well known in the art. Techniques suitable for use in the following examples may be found as set out in Manual of Methods for General
10 Bacteriology (Phillipp Gerhardt, R. G. E. Murray, Ralph N. Costilow, Eugene W. Nester, Willis A. Wood, Noel R. Krieg and G. Briggs Phillips, eds), American Society for Microbiology, Washington, DC. (1994)) or by Thomas D. Brock in Biotechnology: A Textbook of Industrial Microbiology, Second Edition, Sinauer Associates, Inc., Sunderland, MA (1989). All reagents, restriction enzymes and
15 materials used for the growth and maintenance of bacterial cells were obtained from Aldrich Chemicals (Milwaukee, WI), DIFCO Laboratories (Detroit, MI), GIBCO/BRL (Gaithersburg, MD), or Sigma Chemical Company (St. Louis, MO) unless otherwise specified.

- Manipulations of genetic sequences were accomplished using the suite of
20 programs available from the Genetics Computer Group Inc. (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, WI), DNASTAR (DNASTAR, Inc. 1228 S. Park St. Madison, WI 53715 USA), or the "on-line" Probe Match Program from the Ribosomal Database Project II (Michigan State University, East Lansing, MI). Where any sequence analysis software was used in
25 the following examples, default values were used unless otherwise specified.

The meaning of abbreviations is as follows: "h" means hour(s), "min" means minute(s), "sec" means second(s), "d" means day(s), "mL" means milliliters, "L" means liters.

EXAMPLE 1

- 30 Isolation And Characterization Of Dechlorinating Soil Organisms

- Aquifer core samples were obtained by split spoon sampling at depths ranging from 10 to 80 ft, depending on the depth of the particular aquifer to be tested. The cores were taken in sterile stainless steel cylinders or placed in sterile glass vials. The core samples were immediately shipped to the laboratory at
35 ambient temperatures and under anaerobic conditions. Upon arrival the samples were stored in an anaerobic glove bag (chamber) (Coy Laboratory Products Inc., Ann Arbor, MI), whose atmosphere was 10% H₂, 5% CO₂ and 85% N₂.

The laboratory microcosms were prepared in 250 mL Wheaton bottles (Wheaton Co., Millville, NJ) within the anaerobic chamber. Duplicate microcosms were prepared for the following conditions: Killed Control (live soil autoclaved for 1 hr on 2 consecutive days), Live soil, and Live soil + 0.05% yeast extract. Each microcosm contains 20% soil and 80% BTZ-3 media (NH_4Cl , 4.3 g/L; KH_2PO_4 , 50 g/L; $\text{MgCl}\cdot 6\text{H}_2\text{O}$, 20 g/L; $\text{CaCl}_2\cdot 2\text{H}_2\text{O}$, 1 g/L; HEPES, 50 mM/L; mineral solution, 10 mL/L; resazurin 0.2%, 5 mL/L). The microcosm were filled to top such there was little or no headspace, and then stoppered with Teflon™ lined disks and crimp-sealed with aluminum seals (Wheaton Co., Millville, NJ). The resazurin addition permitted the visualization of low potential anaerobic conditions by a color change from pink to colorless. Each microcosm was spiked with 5 ppm from a PCE or TCE solution saturated in water. The microcosms were incubated on their sides in the anaerobic chamber, in the dark, at ambient room temperature (22°C) for up to 180 days.

Samples were analyzed the next day as time zero (t_0) and then twice a week for the dechlorination of PCE or TCE and the formation of cisDCE, vinyl chloride or methane. All samples were taken in the anaerobic chamber by using a syringe mounted with a 23 gauge needle was use to puncture the Teflon™ septa to obtain a 5 mL liquid sample that was injected into a 10 mL headspace vial. Samples were tested using HP Headspace sampler 7694, HP5890 series II GC (FID detector, HP 5 capillary column #19091J-215), HP3365 Chemstation version A.03.34.

Figure 3 plots the concentration (parts per million; ppm) of chloroethenes in the microcosm medium as a function of time (days) and illustrates the dechlorination of chloroethenes. Dechlorination of PCE to TCE could be detected by GC/FID. Within two days with the formation of cisDCE from the dechlorination of TCE was detected. These results are found in the microcosms that has been amended with 0.05% yeast extract plus minimal salts media (BTZ-3 media). These results can also be seen in the microcosms that are amended with the minimal salts media alone. The difference is the dechlorination is slightly delayed. It takes four days before cisDCE is detected. Degradation of cisDCE would occur over the next two weeks. Vinyl chloride and ethene could only be detected at trace levels. The "Killed" control, did not show degradation of PCE or TCE during the duration of the experiment. Cell growth was shown by increase in the turbidity of the microcosm medium and by microscopic analysis.

EXAMPLE 2

Generation of PCR Primers and Probes for the Amplification and Detection of the *Dehalococcoides Ethenogenes* 16S rRNA Profiled

The detection and sequencing of the *Dehalococcoides ethenogenes*-like organisms used the set of PCR primers are shown in Table 1. The PCR primers were designed using signature sequence regions. To determine the location of these signature sequence, the *Dehalococcoides ethenogenes* sequence (GenBank No. AF004928)[SEQ ID NO:7] was aligned using MEGALIGN (DNASTar, Madison, WI) or Pileup (Genetics Computer Group, Madison, WI) with 16S rRNA sequences from 100 organisms that represent most major domains, families and genera in the major kingdoms of Bacteria and Archaea. The conserved, variable, and highly variable regions could be delineated by boxing off the consensus sequences. Primer candidate sequences were manually picked from the variable and highly variable regions and then their uniqueness was determined by determining their potential as probes to a ribosomal sequence database sequences using the "on-line" Probe Match Program from the Ribosomal Database Project II (<http://www.cme.msu.edu/RDP/html/index.html>) RDPII, Michigan State University, East Lansing, MI). This analysis returned an overview of the matches between a probe and its potential target sequence, as a listing and as a phylogenetic overview. The program results showed the sequences that match the query sequence (if there are such sequences) and also showed sequences that had mismatches, deletions and insertions, citing the number and positions of the aberrations.

The sequences which were unique and passed this test as signature sequences were then designed as either a forward or reverse primer, usually dependent on their position in the sequence. The most unique sequence of the signature sequence (specificity) was designed into the 3' end in either type of primer. The selected primers are shown in Table 1.

The primers were synthesized using standard β -cyanoethyl phosphoramidite coupling chemistry on controlled pore glass (CPG) supports on automated DNA oligonucleotide synthesizer (Applied Biosystems Model 392, Perkin-Elmer, Foster City, CA)

The primers were tested after they were synthesized using PCR on samples taken from microcosms known to have *Dehalococcoides ethenogenes*-like organisms. The PCR products were sized on agarose electrophoresis and then cloned and sequenced to verify that the amplified sequences were *Dehalococcoides ethenogenes*-like 16S rRNA sequences.

TABLE 1Primers for *Dehalococcoides ethenogenes*

FP DHE 32	5'AAG TCGAACGGTCTTAAGCA3' SEQ ID NO:9
RP DHE422	5' CGTCATTATTCTTCCCTGTG 3' SEQ ID NO:10
FP DHE 958	5'GGGAAACGACCTGTTAAGTCA 3' SEQ ID NO:11
RP DHE 1212	5'GGATTAGCTCCAGTTCACACTG 3' SEQ ID NO:12
RP DHE 1076	5'AAATTTAAGTAGCAACAAGG 3' SEQ ID NO:13
FP DHE 795	5'GGAGTATCGACCCTCTCTG 3' SEQ ID NO:14
FP DHE 774	5'GGGAGTATCGACCCTCTC 3' SEQ ID NO:15
FP DHE 946	5'AGTGAACCGAAAGGGAAA 3' SEQ ID NO:16
FP DHE 385	5'GGGTTGTAAACCTCTTTTCAC 3' SEQ ID NO:17
RP DHE 806	5'GTTAGCTTCGGCACAGAGAG 3' SEQ ID NO:18
RP DHE 692	5'TCAGTGACAACCTAGAAAAC 3' SEQ ID NO:19
FP DHE1	5'GATGAACGCTAGCGGCG 3' SEQ ID NO:20
FP DHE 30	5'GTGCCTTATGCATGCAAG 3' SEQ ID NO:21
FP DHE 1187	5' AATAGGTTGCAACAGTGTGAA 3' SEQ ID NO:22
FP DHE 1175	5' AATGGACAGAACAATAGGTTGC 3' SEQ ID NO:23
RP DHE 1381	5' GGCACATCGACTTCAAGTGTT 3' SEQ ID NO:24
RP DHE 1381	5' GGCACATCGACTTCAAGTGTT 3' SEQ ID NO:25
FP DHE 558	5' TAACCGGGACG(AT)GTCATTCA 3' SEQ ID NO:26
FP DHE 593	5' GAGTACAGCAGGAGAAAAC 3' SEQ ID NO:27
RP DHE 1394	5' CCTCCTTGCGGTTGGCACATC 3' SEQ ID NO:28
RP DHE 1090	5' GGCAGTCTCGCTAGAAAAT 3' SEQ ID NO:29

EXAMPLE 3

5 Using the *Dehalococcoides Ethenogenes*-Like Specific Primers
 to Detect These Organisms in Microcosms

Nucleic acids were extracted from the microcosm cultures by a bead mill homogenization procedure, FastDNA Spin Kit for Soil (Bio 101, Vista, CA), that was designed to isolate genomic DNA from all cell types. Approximately 10 mL of the microcosm culture was pelleted and resuspended in 500 ul of the culture media. The resuspended pellet was added to a 2.2 mL conical screw-cap tube containing 1.5 g of three differently sized glass and zirconia/silica beads (106 microns, 710-1180 microns). To the sample tubes, 978 ul of sodium phosphate buffer and 122 ul of MT buffer was added. The tubes were homogenized for 30 seconds at speed 5.5 on a Fast Prep bead mill homogenizer. A clear supernatant was obtained by centrifuging the samples at 14,000 x g for 30 seconds. The supernatant was transferred to a clean microcentrifuge tube and

250 μ L of PPS reagent was added and mixed. The resulting precipitate was pelleted through centrifugation at 14,000 \times g for 5 minutes. The supernatant was transferred to a new microcentrifuge tube and 1 mL of binding matrix was added. The samples were placed on a rotator for 2 minutes and then sat on the benchtop for 3 minutes to allow the settling of the silica matrix. Between 500-700 μ L of the supernatant was removed and discarded. The remaining supernatant was used to resuspend the silica matrix and transferred to a spin filter. The spin filter was centrifuged for 1 minute at 14,000 \times g and the flow-through decanted. The silica matrix was washed with 500 μ L of SEWS-M buffer and centrifuged for 1 minute at 16,000 \times g. The flow through was discarded and any residual buffer in the matrix was removed by a 2 minute centrifugation at 14,000 \times g. The spin filter was placed in a catch tube and air dried for 5 minutes in a biological hood. The genomic DNA was eluted by adding 60 μ L of sterile, deionized water, mixing the matrix and the water together with a pipet tip, and centrifuging for 1 minute at 14,000 \times g.

The 16S rRNA gene for *Dehalococcoides ethenogenes* was detected by PCR amplification and gel electrophoresis. The 16S sequences were amplified using *Dehalococcoides ethenogenes* specific 16S rDNA primers shown in Table 1. All PCR amplifications were performed using the GeneAmp PCR kit with Taq DNA polymerase (PE Applied Biosystems, Branchburg, NJ) in a Perkin Elmer 9600 thermal cycler. Amplification reactions contained 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 10 μ M each deoxynucleoside triphosphate, 20 pmol each primer, 2.5 U of Taq polymerase, and 1 μ L of the genomic extraction diluted 1:10 in a final reaction volume of 50 μ L. The PCR conditions were as follows: 2 minutes of denaturation at 95 $^{\circ}$ C, followed by 30 cycles of 30 seconds at 94 $^{\circ}$ C, 30 seconds at 55 $^{\circ}$ C, 30 seconds at 72 $^{\circ}$ C. 8 μ L of the PCR product was visualized on a 2% agarose gel (SeaKem GTG, FMC BioProducts, Rockland, ME) stained with ethidium bromide.

A direct detection protocol used 1 μ L of the microcosm culture was directly added to the PCR as described previously.

After the *Dehalococcoides ethenogenes*-like sequences were detected in the microcosm developed from contaminated soil, FP DHE 1 (SEQ ID NO:20), RP DHE 1330 (SEQ ID NO:12) were used to amplify a 1212 bp (or 1221 bp) fragment, which was cloned (using the PCR dA/T-Cloning System, Invitrogen, Inc., CA) and sequenced (using Model 377 DNA Sequencer kit and system, Applied Biosystems, Perkin-Elmer, Foster City, CA). The sequence was assembled using the Seqman II program (DNASTAR, Inc., Madison, WI). The 16S rDNA sequence contig formed was compared to 16S rDNA sequences obtained

from microcosms developed from contaminated soils from other sites and the comparison is shown in Figure 4.

Figure 4 shows a gel of amplification products generated from PCR amplification of various *Dehalococcoides ethenogenes* isolated from a number of industrial sites contaminated with either PCE or TCE. All amplifications were carried out using primers SEQ ID NOs:17 paired with 19, and SEQ ID NOs:18 paired with 20. Lanes 1 and 12 carry the molecular weight markers. Lanes 2 and 3 are the PCR products generated from organisms isolated from soil containing PCE. Lanes 4, 5, 6, 7, 8 and 9 are the PCR products from organisms isolated from soil containing TCE. Lanes 10 and 11 contain negative PCR controls. As can be seen by the data all samples were detectable by the primers used.

The contiguous sequences from each site was unique, having 96 to 99% similarity to each other. The differences in the sequence are annotated in Table 2. A major difference exists in the consensus sequence that were obtained from all strains (CS) detected at contaminated sites and the reference sequence represented by the published sequence from strain DHE-195 strain (Table 2). At DHE (CS) positions 1088-1096 (*E. coli* coordinates E1146-E1156) there exists a nine base deletion. The sequence in CS strains reads ATTTTCTAGCGAGACTG (SEQ ID NO:31); in the DHE-195 strain it reads ATTTTCTAGCGAGACTAGCGAGACTG (SEQ ID NO:32) (the double underlined sequence is the sequence deleted in the CS strain sequences. Differences in sequence were found at six other base positions as shown below in Table 2.

TABLE 2

<i>E. coli</i>	DHE No.	DHE-195	DHE-PL	DHE-STF	DHE-DAB	DHE-PIN	DHE-DLL
28	I	I	I	I	I	I	I
107	66	A	A	A	G	G	A
184	144	A	A	G	G	G	G
190	150	T	T	C	C	C	C
198	157	A	A	A	T	T	A
201	160	C	C	T	T	T	T
208	167	T	T	C	C	C	C
217	176	C	C	T	T	T	T
222	181	T	T	T	C	C	T
264	226	T	T	C	T	T	C
267	*229	T	C	C	C	C	C
291+	254	d	d	T	d	d	d
333	*296	G	C	C	C	C	C
420	383	T	T	C	T	T	C
444	407	C	C	C	T	T	C

<i>E. coli</i>	DHE No.	DHE-195	DHE-PL	DHE-STF	DHE-DAB	DHE-PIN	DHE-DLL
542	*481	G 480	d 479+	d 480+	d 479+	d 479+	d 479+
631	571	T 570	T 569	T 570	A 569	A 569	T 569
829	769	G 768	G 767	A 768	G 767	G 767	
933	874	G 873	T 872	G 873	G 872	G 872	G 872
934	875	C 874	T 873	C 874	C 873	C 873	C 873
980	*921	d 919+	C 919	C 920	C 919	C 919	C 919
1003	944	A 942	A 942	A 943	T 942	T 942	A 942
1012	955	C 953	C 953	C 954	T 953	T 953	C 953
1020	963	A 961	A 961	A 962	G 961	G 961	A 961
1039	984	G 982	G 982	G 983	A 982	A 982	G 982
1040	985	T 983	T 983	T 984	C 983	C 983	T 983
1087	*1033	G 103	T 1031	T 1032	T 1031	T 1031	T 1031
1114	*1060	d 1057+	C 1058	C 1059	C 1058	C 1058	C 1058
1144-56	1088-96	1086-94 ACTAGC	d 1085+	d 1086+	d 1085+	d 1085+	d 1085+

Legend: DHE No. = Consensus number; number (+) = last base coordinate before base a deletion; bold (red) bases are indicative of base sequences different from DHE 195; (*), bold bases and blocks cells (base and coordinate) implies sequence of all 16S sequences isolates that are different from DHE 195

What is Claimed is:

1. An isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain selected from the group consisting of:

- (a) SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:30;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS at 65°C; and
- (c) an isolated nucleic acid molecule that is completely complementary to (a) or (b).

2. An isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain selected from the group consisting of:

- (a) SEQ ID NOs:9-29;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS at 65°C; and
- (c) an isolated nucleic acid molecule that is completely complementary to (a) or (b).

3. An isolated 16S rDNA sequence of Claim 1 wherein within the 16S DNA sequence the following bases, taken independently or together are:

base E107=G, base E184=G, base E190=C, E 198=T, E201= T, E208=C, E217=T, E222=C, E264=C, E267=C, E291=T, E333= C, E420=C, E444=T, E631=A, E829=A, E933=T, E934=T, E980=C, E1003=T, E1012=T, E1020=G, E1039=A, E1040=C, E1087=T, and E1114=C.

4. An isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain as set forth in SEQ ID NO:1.

5. An isolated bacterial strain comprising any one of the sequences of Claims 1, 3 or 4 wherein said strain has the ability to dechlorinate chlorinated compounds.

6. A method for identifying a dechlorinating bacterial strain comprising:

- (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds;
- (ii) probing the extracted genomic DNA with a probe derived from any one of the sequences of Claims 1, 2, 3 or 4 under suitable hybridization conditions;

wherein the identification of a hybridizable nucleic acid fragment confirms the presence of a bacteria capable of dechlorinating chlorinated compounds.

7. A method for identifying a dechlorinating bacterial strain comprising:

- (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds; and

- (ii) amplifying the extracted genomic DNA with at least one oligonucleotide primer corresponding to a portion of any one of the sequences of Claims 1, 2, 3 or 4 such that amplification products are generated;

5 wherein the presence of amplification products confirms the presence of a bacteria capable of dechlorinating chlorinated compounds.

8. A method for the dechlorination of chlorinated compounds comprising contacting a chlorinated compound with the isolated bacterial strain of Claim 5 under conditions for the dechlorination to occur.

10 9. A method according to Claim 8 wherein said dechlorinating compound is selected from the group consisting of carbontetrachloride, tetrachloroethene, chloroform, dichloromethane, trichloroethene, dichloroethylene, vinyl chloride, and chloroaromatics.

1/17

FIG. 1-1

DHE seq alignments1.msf MSF: 1223

Name: Deh_eth._(cornell)

Name: Deh_eth._(stf)

Name: Dehal_eth._(pl)._seq

Name: Dehlo_eth._(dll)._seq

Name: Dehlo_eth._(dab).

Name: Dehlo_eth._(pin).seq

//

```

1      Deh_eth._(cornell)      60
      Deh_eth._(stf)
      Dehal_eth._(pl)._seq
      Dehlo_eth._(dll)._seq
      Dehlo_eth._(dab).seq
      Dehlo_eth._(pin).seq
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA
      GATGAACGCTAGCGCGTGCCTTATGCATGCAAGTCGAACGGTCTTAAGCAATTAAGATA

```

```

61      Deh_eth._(cornell)      120
      Deh_eth._(stf)
      Dehal_eth._(pl)._seq
      Dehlo_eth._(dll)._seq
      Dehlo_eth._(dab).seq
      Dehlo_eth._(pin).seq
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA
      GTGGCAACCGGTGAGTAACGGCTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGA

```

```

121      Deh_eth._(cornell)      180
      Deh_eth._(stf)
      Dehal_eth._(pl)._seq
      Dehlo_eth._(dll)._seq
      Dehlo_eth._(dab).seq
      Dehlo_eth._(pin).seq
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGCAAGG
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGCAAGG
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
      AACTGAAGGTAATACCGCATGTGATGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG

```

2/17

FIG. 1-2

```

181      Deh_eth._.(cornell)      240      TGCTTGGTGAGGGGCTTGGCTCCGATTAGCTAGTTGGTGGGGTAAATGGTCTACCAAGGCT
      Deh_eth._.(stf)          TGCTTGGTGAGGGGCTTGGCTCCGATTAGCTAGTTGGTGGGGTAAACGGCCTACCAAGGCT
      Dehal_eth._(pl)._seq      TGCTTGGTGAGGGGCTTGGCTCCGATTAGCTAGTTGGTGGGGTAAATGGCCTACCAAGGCT
      Dehlo_eth._(dll)._seq     TGCTTGGTGAGGGGCTTGGCTCCGATTAGCTAGTTGGTGGGGTAAACGGCCTACCAAGGCT
      Dehlo_eth._(dab).seq      CGCTTGGTGAGGGGCTTGGCTCCGATTAGCTAGTTGGTGGGGTAAATGGCCTACCAAGGCT
      Dehlo_eth._(pin).seq      CGCTTGGTGAGGGGCTTGGCTCCGATTAGCTAGTTGGTGGGGTAAATGGCCTACCAAGGCT

241      Deh_eth._.(cornell)      300      TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG
      Deh_eth._(stf)          TCGATCGGTAGCTTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG
      Dehal_eth._(pl)._seq      TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG
      Dehlo_eth._(dll)._seq     TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG
      Dehlo_eth._(dab).seq      TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG
      Dehlo_eth._(pin).seq      TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG

301      Deh_eth._.(cornell)      360      ACTCCTACGGGAGGCAGCAAGGAATCTTGGGCAATGGGCGAAAGCCTGACCCAGCAA
      Deh_eth._(stf)          ACTCCTACGGGAGGCAGCAAGGAATCTTGGGCAATGGGCGAAAGCCTGACCCAGCAA
      Dehal_eth._(pl)._seq      ACTCCTACGGGAGGCAGCAAGGAATCTTGGGCAATGGGCGAAAGCCTGACCCAGCAA
      Dehlo_eth._(dll)._seq     ACTCCTACGGGAGGCAGCAAGGAATCTTGGGCAATGGGCGAAAGCCTGACCCAGCAA
      Dehlo_eth._(dab).seq      ACTCCTACGGGAGGCAGCAAGGAATCTTGGGCAATGGGCGAAAGCCTGACCCAGCAA
      Dehlo_eth._(pin).seq      ACTCCTACGGGAGGCAGCAAGGAATCTTGGGCAATGGGCGAAAGCCTGACCCAGCAA

361      Deh_eth._.(cornell)      420      CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTTCACAGGGAAGAATAATG
      Deh_eth._(stf)          CGCCGCGTGAGGGATGAAGGCTCTCGGGTTGTAAACCTCTTTTTCACAGGGAAGAATAATG
      Dehal_eth._(pl)._seq      CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTTCACAGGGAAGAATAATG
      Dehlo_eth._(dll)._seq     CGCCGCGTGAGGGATGAAGGCTCTCGGGTTGTAAACCTCTTTTTCACAGGGAAGAATAATG
      Dehlo_eth._(dab).seq      CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTTCACAGGGAAGAATAATG
      Dehlo_eth._(pin).seq      CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTTCATAGGGAAGAATAATG

```

3/17

FIG. 1-3

421 Deh_eth._(cornell) 480
 Deh_eth._(stf) ACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGG
 Dehal_eth._(pl)..seq ACGGTACCTGTGGAATAAGCTTCGGCTAACTA CGTGCCAGCAGCCGCGGTAATACGTAGG
 Dehlo_eth._(dll)..seq ACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGG
 Dehlo_eth._(dab)..seq ACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGG
 Dehlo_eth._(pin)..seq ACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGG

481 540
 Deh_eth._(cornell) GAAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTCAAGTTG
 Deh_eth._(stf) .AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTCAAGTTG
 Dehal_eth._(pl)..seq .AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTCAAGTTG
 Dehlo_eth._(dll)..seq .AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTCAAGTTG
 Dehlo_eth._(dab)..seq .AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTCAAGTTG
 Dehlo_eth._(pin)..seq .AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTCAAGTTG

541 600
 Deh_eth._(cornell) GATGTGAAATTTCCCGGCTTAAACCGGGACGTGTCAATCAATACTGTTGGACTAGAGTACA
 Deh_eth._(stf) GATGTGAAATTTCCCGGCTTAAACCGGGACGTGTCAATCAATACTGTTGGACTAGAGTACA
 Dehal_eth._(pl)..seq GATGTGAAATTTCCCGGCTTAAACCGGGACGTGTCAATCAATACTGTTGGACTAGAGTACA
 Dehlo_eth._(dll)..seq GATGTGAAATTTCCCGGCTTAAACCGGGACGTGTCAATCAATACTGTTGGACTAGAGTACA
 Dehlo_eth._(dab)..seq GATGTGAAATTTCCCGGCTTAAACCGGGACGTGTCAATCAATACTGTTGGACTAGAGTACA
 Dehlo_eth._(pin)..seq GATGTGAAATTTCCCGGCTTAAACCGGGACGTGTCAATCAATACTGTTGGACTAGAGTACA

601 660
 Deh_eth._(cornell) GCAGGAGAAAACCGGAATTCCTGGGTGTAGTGGTAAAATGCGTAGATATCGGGAGGAACACC
 Deh_eth._(stf) GCAGGAGAAAACCGGAATTCCTGGGTGTAGTGGTAAAATGCGTAGATATCGGGAGGAACACC
 Dehal_eth._(pl)..seq GCAGGAGAAAACCGGAATTCCTGGGTGTAGTGGTAAAATGCGTAGATATCGGGAGGAACACC
 Dehlo_eth._(dll)..seq GCAGGAGAAAACCGGAATTCCTGGGTGTAGTGGTAAAATGCGTAGATATCGGGAGGAACACC
 Dehlo_eth._(dab)..seq GCAGGAGAAAACCGGAATTCCTGGGTGTAGTGGTAAAATGCGTAGATATCGGGAGGAACACC
 Dehlo_eth._(pin)..seq GCAGGAGAAAACCGGAATTCCTGGGTGTAGTGGTAAAATGCGTAGATATCGGGAGGAACACC

FIG. 1-4

661 Deh_eth._.(cornell) 720
 AGAGCGGAAGGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGGGGAGCG
 Deh_eth._.(stf) AGAGCGGAAGGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGGGGAGCG
 Dehal_eth._(pl)..seq AGAGCGGAAGGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGGGGAGCG
 Dehlo_eth._(dll)..seq AGAGCGGAAGGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGGGGAGCG
 Dehlo_eth._(dab).seq AGAGCGGAAGGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGGGGAGCG
 Dehlo_eth._(pin).seq AGAGCGGAAGGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGGGGAGCG

721 780
 AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT
 Deh_eth._.(cornell) AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT
 Deh_eth._.(stf) AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT
 Dehal_eth._(pl)..seq AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT
 Dehlo_eth._(dll)..seq AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT
 Dehlo_eth._(dab).seq AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT
 Dehlo_eth._(pin).seq AACAGAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATAGGGAGT

781 840
 ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC
 Deh_eth._.(cornell) ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC
 Deh_eth._.(stf) ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC
 Dehal_eth._(pl)..seq ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC
 Dehlo_eth._(dll)..seq ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC
 Dehlo_eth._(dab).seq ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC
 Dehlo_eth._(pin).seq ATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTACGGTCGC

841 900
 AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA
 Deh_eth._.(cornell) AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA
 Deh_eth._.(stf) AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA
 Dehal_eth._(pl)..seq AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA
 Dehlo_eth._(dll)..seq AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA
 Dehlo_eth._(dab).seq AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA
 Dehlo_eth._(pin).seq AAGGCTAAAACTCAAAGGAATTACGGGGGCCCGCACAAAGCAGCGGAGCGTGTGGTTTAA

5/17

FIG. 1-5

901 Deh_eth._ (cornell) 960
 Deh_eth._ (stf) TTCTGATGCTACACGAAGAAC.TTACCAAGATTTGACATGCATGAAGTAGTGAACCGAAAG
 Dehal_eth._ (pl)._seq TTCTGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAACCGAAAG
 Dehlo_eth._ (dll)._seq TTCTGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAACCGAAAG
 Dehlo_eth._ (dab)._seq TTCTGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAACCGAAAG
 Dehlo_eth._ (pin)._seq TTCTGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAACCGAAAG

961 1020
 Deh_eth._ (cornell) GGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGCTCAGCTCGTG
 Deh_eth._ (stf) GGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGCTCAGCTCGTG
 Dehal_eth._ (pl)._seq GGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGCTCAGCTCGTG
 Dehlo_eth._ (dll)._seq GGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGCTCAGCTCGTG
 Dehlo_eth._ (dab)._seq GGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGCTCAGCTCGTG
 Dehlo_eth._ (pin)._seq GGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGCTCAGCTCGTG

1021 1080
 Deh_eth._ (cornell) CCGTGAGGTGTTGGTTAAGTCCTGCAACGAGCGCAACC.TTGTGCTAGTTAAATTTTC
 Deh_eth._ (stf) CCGTGAGGTGTTGGTTAAGTCCTGCAACGAGCGCAACCCTTGTGCTAGTTAAATTTTC
 Dehal_eth._ (pl)._seq CCGTGAGGTGTTGGTTAAGTCCTGCAACGAGCGCAACCCTTGTGCTAGTTAAATTTTC
 Dehlo_eth._ (dll)._seq CCGTGAGGTGTTGGTTAAGTCCTGCAACGAGCGCAACCCTTGTGCTAGTTAAATTTTC
 Dehlo_eth._ (dab)._seq CCGTGAGGTGTTGGTTAAGTCCTGCAACGAGCGCAACCCTTGTGCTAGTTAAATTTTC
 Dehlo_eth._ (pin)._seq CCGTGAGGTGTTGGTTAAGTCCTGCAACGAGCGCAACCCTTGTGCTAGTTAAATTTTC

1081 1140
 Deh_eth._ (cornell) TAGCGAGACTAGCGAGACTGCCCCCGGAAACGGGGAGGAAGGTGGGGATGACGTCAAGTC
 Deh_eth._ (stf) TAGCGAG.....ACTGCCCCCGGAAACGGGGAGGAAGGTGGGGATGACGTCAAGTC
 Dehal_eth._ (pl)._seq TAGCGAG.....ACTGCCCCCGGAAACGGGGAGGAAGGTGGGGATGACGTCAAGTC
 Dehlo_eth._ (dll)._seq TAGCGAG.....ACTGCCCCCGGAAACGGGGAGGAAGGTGGGGATGACGTCAAGTC
 Dehlo_eth._ (dab)._seq TAGCGAG.....ACTGCCCCCGGAAACGGGGAGGAAGGTGGGGATGACGTCAAGTC
 Dehlo_eth._ (pin)._seq TAGCGAG.....ACTGCCCCCGGAAACGGGGAGGAAGGTGGGGATGACGTCAAGTC

FIG. 1-6

Deh_eth._.(cornell)	1141	AGCATGGCCCTTTATATCTTGGGCTACACACACGCTACAATGGACAGAACAAATAGGTTGCA	1200
Deh_eth._.(stf)		AGCATGGCCCTTTATATCTTGGGCTACACACACGCTACAATGGACAGAACAAATAGGTTGCA	
Dehal_eth._(pl)..seq		AGCATGGCCCTTTATATCTTGGGCTACACACACGCTACAATGGACAGAACAAATAGGTTGCA	
Dehlo_eth._(dll)..seq		AGCATGGCCCTTTATATCTTGGGCTACACACACGCTACAATGGACAGAACAAATAGGTTGCA	
Dehlo_eth._(dab).seq		AGCATGGCCCTTTATATCTTGGGCTACACACACGCTACAATGGACAGAACAAATAGGTTGCA	
Dehlo_eth._(pin).seq		AGCATGGCCCTTTATATCTTGGGCTACACACACGCTACAATGGACAGAACAAATAGGTTGCA	

Deh_eth._.(cornell)	1201	ACAGTGTGAACTGGAGCTAATCC	1223	Seq. I.D. No 7
Deh_eth._(stf)		ACAGTGTGAACTGGAGCTAATCC		Seq. I.D. No.3
Dehal_eth._(pl)..seq		ACAGTGTGAACTGGAGCTAATCC		Seq. I.D. No.2
Dehlo_eth._(dll)..seq		ACAGTGTGAACTGGAGCTAATCC		Seq. I.D. No.6
Dehlo_eth._(dab).seq		ACAGTGTGAACTGGAGCTAATCC		Seq. I.D. No.4
Dehlo_eth._(pin).seq		ACAGTGTGAACTGGAGCTAATCC		Seq. I.D. No.5

7/17

FIG. 2-1

```

12/10/98BEcAlignmentG.msf  MSF: 1576
Name: E.coli.rnaB                      Len: 1542
Name: Deh_eth._(cornell)              Len: 1443 DHE-195
Name: Deh_eth._(stf)                  Len: 1212 STFD
Name: Dehal_eth._(pl)._seq           Len: 1212
Name: Dehlo_eth._(dab).seq           Len: 1212
Name: Dehlo_eth._(pin).seq           Len: 1212
Name: Dehlo_eth._(dll).seq           Len: 1212
//

1
E.coli.rnaB                      60
Deh_eth._(cornell)              AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGACGGCCTAACACATGCAA
Deh_eth._(stf)                  .....GATGAACGCTAGCGGCGTGCCTTATGCATGCAA
Dehal_eth._(pl)._seq           .....GATGAACGCTAGCGGCGTGCCTTATGCATGCAA
Dehlo_eth._(dab).seq           .....GATGAACGCTAGCGGCGTGCCTTATGCATGCAA
Dehlo_eth._(pin).seq           .....GATGAACGCTAGCGGCGTGCCTTATGCATGCAA
Dehlo_eth._(dll).seq           .....GATGAACGCTAGCGGCGTGCCTTATGCATGCAA

61
E.coli.rnaB                      120
Deh_eth._(cornell)              GTCGAACGGTAACAGGAAGAGCTTGCTTCTTGCTGACGAGTGGCGGACGGGTGAGTAA
Deh_eth._(stf)                  GTCGAACGGTCTTAAGCAA...TTAA.....GAT.AGTGGCAAACGGGTGAGTAA
Dehal_eth._(pl)._seq           GTCGAACGGTCTTAAGCAA...TTAA.....GAT.AGTGGCAAACGGGTGAGTAA
Dehlo_eth._(dab).seq           GTCGAACGGTCTTAAGCAA...TTAA.....GAT.AGTGGCAAACGGGTGAGTAA
Dehlo_eth._(pin).seq           GTCGAACGGTCTTAAGCAA...TTAA.....GAT.AGTGGCAAACGGGTGAGTAA
Dehlo_eth._(dll).seq           GTCGAACGGTCTTAAGCAA...TTAA.....GAT.AGTGGCAAACGGGTGAGTAA

```

8/17

FIG. 2-2

121 179
E. coli. rrnaB TGTCTGGGAAC.TGCCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCA
 Deh_eth._(cornell) CGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAAGGTAATACCGCA
 Deh_eth._(stf) CGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAAGGTAATACCGCA
 Dehal_eth._(pl).seq CGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAAGGTAATACCGCA
 Dehlo_eth._(dab).seq CGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAAGGTAATACCGCA
 Dehlo_eth._(pin).seq CGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAAGGTAATACCGCA
 Dehlo_eth._(dll).seq CGCGTAAGTAACCTACCTCTAAGTGGGGGATAGCTTCGGGAAACTGAAGGTAATACCGCA

180 236
E. coli. rrnaB TAACGTCGCAAGACCAAGAGGGGGACCTTCGGGCCCTCTTGCCATCGGATGTG...CCCA
 Deh_eth._(cornell) TGTGATGGGCTGAC.ATAAGTCGGTTCATTAAAGCCGCAAGGTGCTTGGTGAGGGGCTTG
 Deh_eth._(stf) TGTGGTGGGCCGAC.ATAAGTTGGTTCACATAAGCCGTAAGGTGCTTGGTGAGGGGCTTG
 Dehal_eth._(pl).seq TGTGATGGGCTGAC.ATAAGTCGGTTCATTAAAGCCGCAAGGTGCTTGGTGAGGGGCTTG
 Dehlo_eth._(dab).seq TGTGGTGGGCCGAC.ATATGTTGGTTCACATAAGCCGTAAGGGCTTGGTGAGGGGCTTG
 Dehlo_eth._(pin).seq TGTGGTGGGCCGAC.ATATGTTGGTTCACATAAGCCGTAAGGGCTTGGTGAGGGGCTTG
 Dehlo_eth._(dll).seq TGTGGTGGGCCGAC.ATAAGTTGGTTCACATAAGCCGTAAGGTGCTTGGTGAGGGGCTTG

237 295
E. coli. rrnaB GATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCT.GGTC
 Deh_eth._(cornell) CGTCCGATTAGCTAGTTGGTGGGGTAATGGTCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Deh_eth._(stf) CGTCCGATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCTTCGATCGGTAGCTTGGTC
 Dehal_eth._(pl).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCCCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo_eth._(dab).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCCCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo_eth._(pin).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCCCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo_eth._(dll).seq CGTCCGATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCTTCGATCGGTAGCT.GGTC

9/17

FIG. 2-3

296 E.coli.rnaB 355
 Deh_eth._(cornell) TGAGAGGATGACCAGCCACACTGGAAC TGAGACACGGTCCAGACTCCTACGGGAGGCAGC
 Deh_eth._(stf) TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGGAGGCAGC
 Dehal_eth._(pl).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGGAGGCAGC
 Dehlo_eth._(dab).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGGAGGCAGC
 Dehlo_eth._(pin).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGGAGGCAGC
 Dehlo_eth._(dll).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGGAGGCAGC

356 415
 E.coli.rnaB AGTGGGGAATATTGCACAAATGGGGCGAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAA
 Deh_eth._(cornell) AGCAAGGAATCTTGGCAATGGGGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Deh_eth._(stf) AGCAAGGAATCTTGGCAATGGGGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehal_eth._(pl).seq AGCAAGGAATCTTGGCAATGGGGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehlo_eth._(dab).seq AGCAAGGAATCTTGGCAATGGGGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehlo_eth._(pin).seq AGCAAGGAATCTTGGCAATGGGGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehlo_eth._(dll).seq AGCAAGGAATCTTGGCAATGGGGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA

416 475
 E.coli.rnaB GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGGAGTAAAGTTAATACCTTTGCG
 Deh_eth._(cornell) GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGAA.....TAAT.....
 Deh_eth._(stf) GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGAA.....TAAT.....
 Dehal_eth._(pl).seq GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGAA.....TAAT.....
 Dehlo_eth._(dab).seq GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGAA.....TAAT.....
 Dehlo_eth._(pin).seq GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGAA.....TAAT.....
 Dehlo_eth._(dll).seq GGCTTCGGGTGTAAAGTACTTTCAGCGGGGAGGAAGAA.....TAAT.....

10/17

FIG. 2-4

```

476      E.coli.rnaB      535      TCATTGACGTTACCCGAGAAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGTAATA
      Deh_eth._.(cornell)      ....GACGGTACCTGTGGAATAAGCTTCGGCTAACCTACGTGCCAGCAGCCGCGTAATA
      Deh_eth._.(stf)      ....GACGGTACCTGTGGAATAAGCTTCGGCTAACCTACGTGCCAGCAGCCGCGTAATA
      Dehal_eth._(pl)._seq      ....GACGGTACCTGTGGAATAAGCTTCGGCTAACCTACGTGCCAGCAGCCGCGTAATA
      Dehlo_eth._(dab).seq      ....GACGGTACCTGTGGAATAAGCTTCGGCTAACCTACGTGCCAGCAGCCGCGTAATA
      Dehlo_eth._(pin).seq      ....GACGGTACCTGTGGAATAAGCTTCGGCTAACCTACGTGCCAGCAGCCGCGTAATA
      Dehlo_eth._(dll).seq      ....GACGGTACCTGTGGAATAAGCTTCGGCTAACCTACGTGCCAGCAGCCGCGTAATA

536      E.coli.rnaB      594      CGGAGGGT.GCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGAGCGGTTGT
      Deh_eth._.(cornell)      CGTAGGGAAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTC
      Deh_eth._(stf)      CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTC
      Dehal_eth._(pl)._seq      CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTC
      Dehlo_eth._(dab).seq      CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTC
      Dehlo_eth._(pin).seq      CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTC
      Dehlo_eth._(dll).seq      CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGGCGTAAAGTGAGCGTAGGTGGTCTTTC

595      E.coli.rnaB      654      AAGTCAGATGTGAAATCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTTG
      Deh_eth._.(cornell)      AAGTTGGATGTGAAATTTCCCGGCTTAACCCGGACGTGTCAATCAATCTGTGGACTAG
      Deh_eth._(stf)      AAGTTGGATGTGAAATTTCCCGGCTTAACCCGGACGTGTCAATCAATCTGTGGACTAG
      Dehal_eth._(pl)._seq      AAGTTGGATGTGAAATTTCCCGGCTTAACCCGGACGTGTCAATCAATCTGTGGACTAG
      Dehlo_eth._(dab).seq      AAGTTGGATGTGAAATTTCCCGGCTTAACCCGGACGTGTCAATCAATCTGTGGACTAG
      Dehlo_eth._(pin).seq      AAGTTGGATGTGAAATTTCCCGGCTTAACCCGGACGTGTCAATCAATCTGTGGACTAG
      Dehlo_eth._(dll).seq      AAGTTGGATGTGAAATTTCCCGGCTTAACCCGGACGTGTCAATCAATCTGTGGACTAG

```

11/17

FIG. 2-5

```

655      E.coli.rnaB      714
      Deh_eth._(cornell) AGTCTCGTAGAGGGGGTAGAATTCACGGTGTAGCGGTGAAATCGGTAGAGATCTGGAGG
      Deh_eth._(stf) AGTACAGCAGGAGAAACGGAATTCCTGGTGTAGTGGTAAATGCGTAGATATCGGGAGG
      Dehal_eth._(pl).seq AGTACAGCAGGAGAGAAACGGAATTCCTGGTGTAGTGGTAAATGCGTAGATATCGGGAGG
      Dehlo_eth.(dab).seq AGTACAGCAGGAGAGAAACGGAATTCCTGGTGTAGTGGTAAATGCGTAGATATCGGGAGG
      Dehlo_eth.(pin).seq AGTACAGCAGGAGAGAGAAACGGAATTCCTGGTGTAGTGGTAAATGCGTAGATATCGGGAGG
      Dehlo_eth.(dll).seq AGTACAGCAGGAGAGAGAAACGGAATTCCTGGTGTAGTGGTAAATGCGTAGATATCGGGAGG

715      E.coli.rnaB      774
      Deh_eth._(cornell) AATACCGGTGGCGAAGGGGGCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGG
      Deh_eth._(stf) AACACCAGAGGCGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
      Dehal_eth._(pl).seq AACACCAGAGGCGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
      Dehlo_eth.(dab).seq AACACCAGAGGCGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
      Dehlo_eth.(pin).seq AACACCAGAGGCGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
      Dehlo_eth.(dll).seq AACACCAGAGGCGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG

755      E.coli.rnaB      834
      Deh_eth._(cornell) GGAGCAAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGT
      Deh_eth._(stf) GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATA
      Dehal_eth._(pl).seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATA
      Dehlo_eth.(dab).seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATA
      Dehlo_eth.(pin).seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATA
      Dehlo_eth.(dll).seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTAAACTATGGACACTAGGTATA

```


FIG. 2-6

835 E.coli.rnaB TGTCCTTGGGGTGGCTT.CCGAGCTAACGGTTAAGTCGACCGCCTGGGGAGTAC 893
 Deh_eth._(cornell) GGGAGTATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTAC
 Deh_eth._(stf) GGGAGTATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTAC
 Dehal._eth._(pl)._seq GGGAGTATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTAC
 Dehlo._eth._(dab).seq GGGAGTATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTAC
 Dehlo._eth._(pin).seq GGGAGTATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTAC
 Dehlo._eth._(dll).seq GGGAGTATCGACCCCTCTGTGCCGAAGCTAACGCTTAAAGTGTCGCCCTGGGGAGTAC

901 E.coli.rnaB GGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCCGACAAAGCGGTGGAGCATGTG 953
 Deh_eth._(cornell) GGTCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGCGAGCGTGTG
 Deh_eth._(stf) GGTCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGCGAGCGTGTG
 Dehal._eth._(pl)._seq GGTCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGCGAGCGTGTG
 Dehlo._eth._(dab).seq GGTCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGCGAGCGTGTG
 Dehlo._eth._(pin).seq GGTCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGCGAGCGTGTG
 Dehlo._eth._(dll).seq GGTCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGCGAGCGTGTG

954 E.coli.rnaB GTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGA..AGTTTTC 1011
 Deh_eth._(cornell) GTTTAATTCGATGCTACACGAAGAAC.TTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Deh_eth._(stf) GTTTAATTCGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehal._eth._(pl)._seq GTTTAATTCGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehlo._eth._(dab).seq GTTTAATTCGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehlo._eth._(pin).seq GTTTAATTCGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehlo._eth._(dll).seq GTTTAATTCGATGCTACACGAAGAACCCTTACCAAGATTTGACATGCATGAAGTAGTGAAC

12/17

13/17

FIG. 2-7

1012
E. coli. rnaB AGAGATGAGAAATGTCCTTCGGG. AACCGTGAG. ACAGGTGCTGCATGGCTGTCGTCAG 1068
 Deh_eth._(cornell) CGAAAGGGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGTCGTCAG
 Deh_eth._(stf) CGAAAGGGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGTCGTCAG
 Dehal_eth._(pl).seq CGAAAGGGAAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGTCGTCAG
 Dehlo_eth._(dab).seq TGAAAGGGGAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGTCGTCAG
 Dehlo_eth._(pin).seq TGAAAGGGGAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGTCGTCAG
 Dehlo_eth._(dll).seq CGAAAGGGGAACGACCTGTTAAGTCAGGAGTTTGACAGGTGCTGCATGGCTGTCGTCAG

1069
E. coli. rnaB CTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC 1128
 Deh_eth._(cornell) CTCGTGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Deh_eth._(stf) CTCGTGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehal_eth._(pl).seq CTCGTGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehlo_eth._(dab).seq CTCGTGCCGTGAGGTGTTGGTAAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehlo_eth._(pin).seq CTCGTGCCGTGAGGTGTTGGTAAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehlo_eth._(dll).seq CTCGTGCCGTGAGGTGTTGGTAAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC

1129
E. coli. rnaB CAGCGGTCCGGCCGGGAACCTCAAAGGAGACTGCCAGTGATAAACTGG. AGGAAGTGGGG 1187
 Deh_eth._(cornell) .AATTTTCTAGC.GAG.ACT..AGCGAGACTGCCC.CGCGAAACGGGGAGGAAGGTGGGG
 Deh_eth._(stf) .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGGAGGAAGGTGGGG
 Dehal_eth._(pl).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGGAGGAAGGTGGGG
 Dehlo_eth._(dab).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGGAGGAAGGTGGGG
 Dehlo_eth._(pin).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGGAGGAAGGTGGGG
 Dehlo_eth._(dll).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGGAGGAAGGTGGGG

14/17

FIG. 2-8

1188
 E.coli.rnaB 1247
 Deh_eth._(cornell) ATGACGTCAAGTCATCATGGCCCTTACGACCGGCTACACACGCTGCTACAAATGGCGCAT
 Deh_eth._(stf) ATGACGTCAAGTCAGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAAATGGACAGA
 Dehal_eth._(pl).seq ATGACGTCAAGTCAGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAAATGGACAGA
 Dehlo_eth.(dab).seq ATGACGTCAAGTCAGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAAATGGACAGA
 Dehlo_eth.(pin).seq ATGACGTCAAGTCAGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAAATGGACAGA
 Dehlo_eth.(dll).seq ATGACGTCAAGTCAGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAAATGGACAGA

1248
 E.coli.rnaB 1307
 Deh_eth._(cornell) ACAAGAGAGGAGCGACCTCGGAGAGCAAGCGGACCTCATAAAGTGGTGTAGTCCGGAT
 Deh_eth._(stf) ACAATAGGTTGCAACAGTGTGAACCTGGAGCTAATCCT.CAAAGCTGTCTCAGTTCGGAT
 Dehal_eth._(pl).seq ACAATAGGTTGCAACAGTGTGAACCTGGAGCTAATCC
 Dehlo_eth.(dab).seq ACAATAGGTTGCAACAGTGTGAACCTGGAGCTAATCC
 Dehlo_eth.(pin).seq ACAATAGGTTGCAACAGTGTGAACCTGGAGCTAATCC
 Dehlo_eth.(dll).seq ACAATAGGTTGCAACAGTGTGAACCTGGAGCTAATCC

1308
 E.coli.rnaB 1367
 Deh_eth._(cornell) TGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAAATGCC
 Deh_eth._(stf) TGCAGGCTGAACCCGCCCTGCATGAAGTTGGAGTTGCTAGTAACCGCATATCAGCAAGGT
 Dehal_eth._(pl).seq
 Dehlo_eth.(dab).seq
 Dehlo_eth.(pin).seq
 Dehlo_eth.(dll).seq

15/17

FIG. 2-9

1368	E.coli.rnaB	ACGGTGAATACGTTCCCGGCCCTTGTAACACACCGCCCGTCACACCATGGGAGTGGGTGTC	1437
	Deh_eth._(cornell)	GCGGTGAATACGTTCTCGGGCCTTGTAACACACCGCCCGTCACGTCATGANAGCCCGTAAC	
	Deh_eth._(stf)	GCGGTGAATACGTTCTCGGGCCTTGTAACACACCGCCCGT	
	Dehal_eth._(pl).seq		
	Dehlo_eth._(dab).seq		
	Dehlo_eth._(pin).seq		
	Dehlo_eth._(dll).seq		
1438	E.coli.rnaB	AAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACCTTGTGATTCATGACTGG	1487
	Deh_eth._(cornell)	ACTTGAAGTCGATGTGCCAACCCGAAGGAGGCAGTCGCCGAGGGTGGGACTGGTAATTGG	
	Deh_eth._(stf)		
	Dehal_eth._(pl).seq		
	Dehlo_eth._(dab).seq		
	Dehlo_eth._(pin).seq		
	Dehlo_eth._(dll).seq		
1488	E.coli.rnaB	GGTGAAGTCGTAACAAGGTAACCGTAGGGGAACCTGCGGTTGGATCACCTCCTTA	1542
	Deh_eth._(cornell)	GACGAAGTCGTAACAAGTA	
	Deh_eth._(stf)		
	Dehal_eth._(pl).seq		
	Dehlo_eth._(dab).seq		
	Dehlo_eth._(pin).seq		
	Dehlo_eth._(dll).seq		
		Seq. I.D. No.33	
		Seq. I.D. No.7	
		Seq. I.D. No.3	
		Seq. I.D. No.2	
		Seq. I.D. No.4	
		Seq. I.D. No.5	
		Seq. I.D. No.6	

16/17

PCE
TCE
DCE
VC

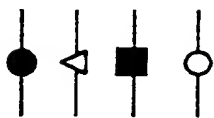
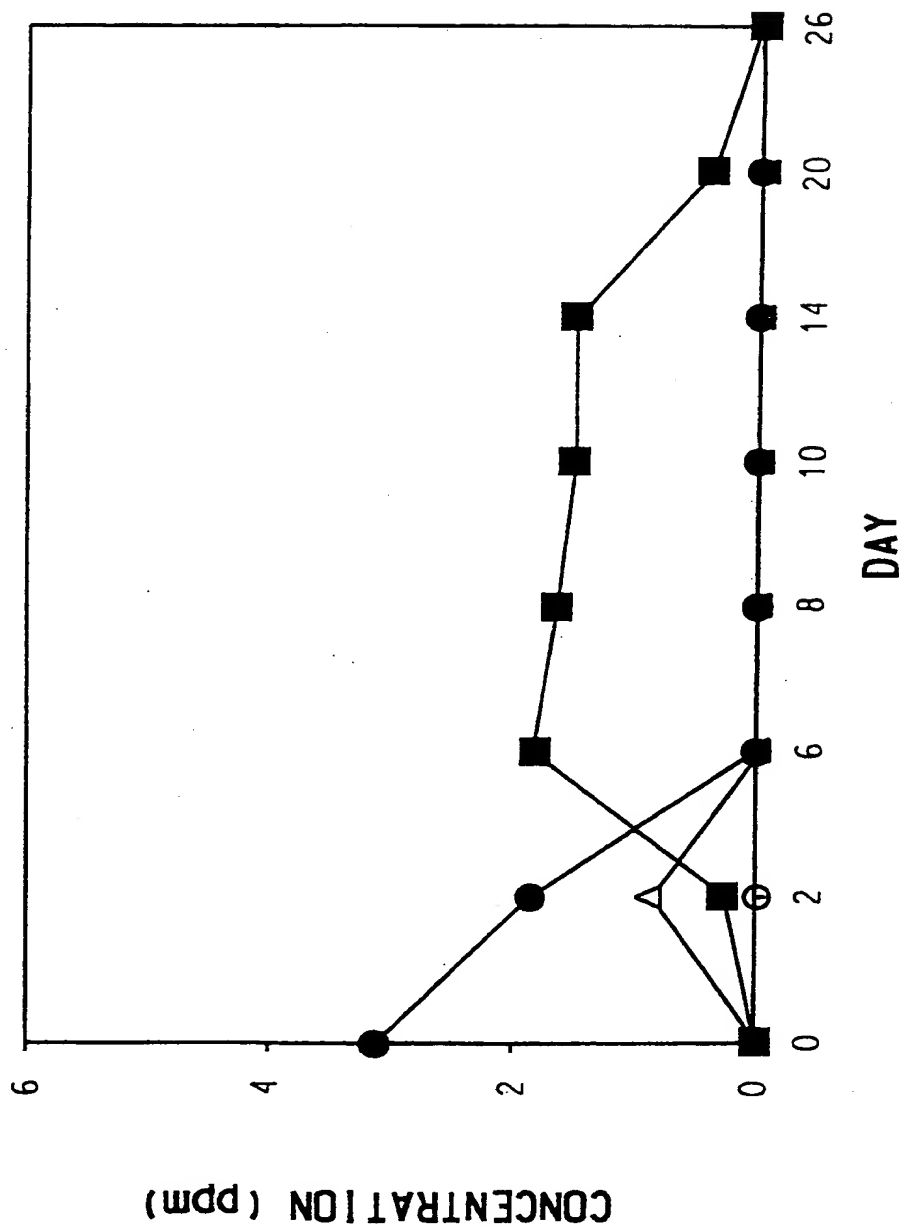
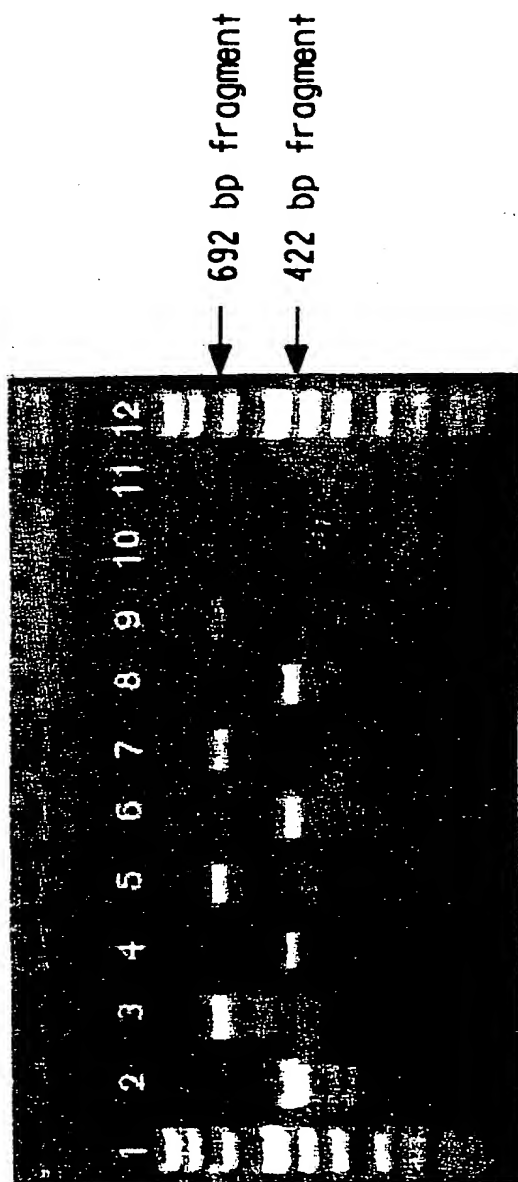


FIG. 3



17/17

FIG. 4



SEQUENCE LISTING

<110> E. I. DU PONT DE NEMOURS AND COMPANY

<120> NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF
DECHLORINATING BACTERIA

<130> BC1002 PCT

<140>

<141>

<150> 60/129,511

<151> 1999-04-15

<160> 33

<170> Microsoft Office 97

<210> 1

<211> 24

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 1

atttttctagc gagactgccc cgcg

24

<210> 2

<211> 1212

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 2

gatgaacgct	agcggcgctgc	cttatgcatg	caagtcgaac	ggtcttaagc	aattaagata	60
gtggcaaacg	ggtgagtaac	gcgtaagtaa	cctacctcta	agtgggggat	agcttcggga	120
aactgaagg	aataccgcat	gtgatgggct	gacataagtc	ggttcattaa	agccgcaagg	180
tgcttggtga	ggggcttgcg	tccgattagc	tagttgggtg	ggtaatggcc	taccaaggct	240
tcgatcggta	gctggtctga	gaggatgatc	agccacactg	ggactgagac	acggcccaga	300
ctcctacggg	aggcagcagc	aaggaatctt	gggcaatggg	cgaaagcctg	accagcaaac	360
gccgcgtgag	ggatgaaggc	tttcgggttg	taaacctctt	ttcacaggga	agaataatga	420
cggtacctgt	ggaataagct	tcggctaact	acgtgccagc	agccgcggta	atacgtagga	480
agcaagcggt	atccggattt	attgggcgta	aagtgcgcgt	aggtgggtctt	tcaagttgga	540
tgtgaaattt	cccggcttaa	ccgggacgtg	tcattcaata	ctggtggact	agagtacagc	600
aggagaaaac	ggaattcccg	gtgtagtgg	aaaatgcgta	gatatcgggg	ggaacaccag	660
aggcgaaggc	ggttttctag	gttgctactg	acactgaggc	tcgaaagcgt	ggggagcgaa	720
cagaattaga	tactctggta	gtccacgcct	taaactatgg	acactaggta	tagggagtat	780
cgaccctctc	tgtgccgaag	ctaacgctyt	aagtgtccc	cctggggagt	acggtcgcaa	840
ggctaaaact	caaaggaatt	gacggggg	cttacaagca	gcggagcgtg	tggtttaatt	900
cgatgctaca	cgaagaacct	taccaagatt	tgacatgcat	gaagtagtga	accgaaagg	960
aaacgacctg	ttaagtcagg	agtttgca	ggtgctgcat	ggctgctg	agctcggtg	1020
gtgaggtgtt	tggttaagtc	ctgcaacgag	cgcaaccctt	ggtgctagtt	aaatcttcta	1080
gcgagactgc	cccgcgaaac	ggggaggaag	gtggggatga	cgtcaagtca	gcattggcctt	1140
tatatcttgg	gctacacaca	cgctacaatg	gacagaacaa	taggttgcaa	cagtgtgaac	1200
tggagctaat	cc					1212

<210> 3

<211> 1335

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 3

gatgaacgct	agcggcgctgc	cttatgcatg	caagtcgaac	ggtcttaagc	aattaagata	60
gtggcaaacg	ggtgagtaac	gcgtaagtaa	cctacctcta	agtgggggat	agcttcggga	120
aactgaagg	aataccgcat	gtggtggg	gacataagtt	ggttcactaa	agccgtaagg	180
tgcttggtga	ggggcttgcg	tccgattagc	tagttgggtg	ggtaacggcc	taccaaggct	240
tcgatcggta	gcttgggtctg	agaggatgat	cagccacact	gggactgaga	cacggcccag	300

actcctacgg	gaggcagcag	caaggaatct	tgggcaatgg	gcgaaagcct	gaccagcaa	360
cgccgcgtga	gggatgaagg	ctctcgggtt	gtaaacctct	tttcacaggg	aagaataatg	420
acggtacctg	tggaataagc	ttcggctaac	tacgtgccag	cagccgcggt	aatacgtagg	480
aagcaagcgt	tatccggatt	tattgggcgt	aaagtgagcg	taggtgggtct	ttcaagttgg	540
atgtgaaatt	tcccggctta	accgggacgt	gtcattcaat	actggtggac	tagagtacag	600
caggagaaaa	cggaattccc	ggtgtagtgg	taaaatgcgt	agatatcggg	aggaacacca	660
gaggcgaagg	cggttttcta	ggttgctact	gacactgagg	ctcgaagcgt	tggggagcga	720
acagaattag	atactctggt	agtccacgcc	ttaactatg	gacactaagt	atagggagta	780
tcgaccctct	ctgtgccgaa	gctaacgctt	taagtgtccc	gcctggggag	tacggctcgca	840
aggctaaaac	tcaaaggaat	tgacgggggc	ccgcacaagc	agcggagcgt	gtggtttaat	900
tcgatgctac	acgaagaacc	ttaccaagat	ttgacatgca	tgaagtagtg	aaccgaaagg	960
gaaacgcact	gttaagtcag	gagtttgac	agggtgctgc	tggctgtcgt	cagctcgtgc	1020
cgtgaaggtg	ttggttaagt	cctgcaacga	gcgcaaccct	tgttgctagt	taaattttct	1080
agcgagactg	ccccgcgaaa	cggggaggaa	ggtggggatg	acgtcaagtc	agcatggcct	1140
ttatatcttg	ggctacacac	acgctacaat	ggacagaaca	ataggttgca	acagtgtgaa	1200
ctggagctaa	tcctcaaagc	tgtcctcagt	tcggattgca	ggctgaaacc	cgctgcgtg	1260
aagttggagt	tgctagtaac	cgcataatcag	caaggtgcgg	tgaatacgtt	ctcgggcctt	1320
gtacacaccg	cccgt					1335

<210> 4

<211> 1212

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 4

gatgaacgct	agcggcgtgc	cttatgcatg	caagtcgaac	ggtcttaagc	aattaagata	60
gtggcgaacg	ggtgagtaac	gcgtaagtaa	cctacctcta	agtgggggat	agcttcggga	120
aactgaagg	aataccgcat	gtggtgggccc	gacatatggt	ggttcactaa	agccgtaagg	180
cgcttggtga	ggggcttgcg	tccgattagc	tagttggtgg	ggtaatggcc	taccaaggct	240
tcgatcggtg	gctggtctga	gaggatgatc	agccacactg	ggactgagac	acggcccaga	300
ctcctacggg	aggcagcagc	aaggaatctt	gggcaatggg	cgaaagcctg	acccagcaac	360
gccgcgtgag	ggatgaaggc	tttcgggttg	taaacctctt	ttcataggga	agaataatga	420
cgttacctgt	ggaataagct	tcggctaact	acgtgccagc	agccgcggtg	atacgtagga	480
agcaagcgtt	atccggattt	attgggcgta	aagttagcgt	aggtggtctt	tcaagttgga	540
tgtgaaattt	cccggcttaa	ccgggacgag	tcattcaata	ctggttgact	agagtacagc	600
aggagaaaac	ggaattcccg	gtgtagtgg	aaaatgcgta	gatatcggga	ggaacaccag	660
aggcgaaggc	ggttttctag	gttgtcactg	acactgaggc	tcgaaagcgt	ggggagcgaa	720
cagaattaga	tactctggtg	gtccacgcct	taaactatgg	acactaggtg	tagggagtat	780
cgaccctctc	tgtgccgaag	ctaacgcctt	aagtgtcccg	cctggggagt	acggtcgcaa	840
ggctaaaact	caaaggaatt	gacgggggccc	cgcacaagca	gcggagcgtg	tggtttaatt	900
cgatgctaca	cgaagaacct	taccaagatt	tgacatgcat	gtagtagtga	actgaaaggg	960
gaacgacctg	ttaagtcagg	aacttgacac	ggtgctgcat	ggctgtcgtc	agctcgtgcc	1020
gtgaggtgtt	tgtttaaagtc	ctgcaacgag	cgcaaccctt	gttgctagt	aaattttcta	1080
gcgagactgc	ccccgcgaaa	ggggagggaag	gtggggatga	cgtcaagtca	gcatggcctt	1140
tatatcttgg	gctacacaca	cgctacaatg	gacagaacaa	taggttgcaa	cagtgtgaac	1200
tggagctaatt	cc					1212

<210> 5

<211> 1212

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 5

gatgaacgct	agcggcgtgc	cttatgcatg	caagtcgaac	ggtcttaagc	aattaagata	60
gtggcaaacg	ggtgagtaac	gcgtaagtaa	cctacctcta	agtgggggat	agcttcggga	120
aactgaagg	aataccgcat	gtggtgggccc	gacataagtt	ggttcactaa	agccgtaagg	180
tgcttggtga	ggggcttgcg	tccgattagc	tagttggtgg	ggtaatggcc	taccaaggct	240
tcgatcggtg	gctggtctga	gaggatgatc	agccacactg	ggactgagac	acggcccaga	300
ctcctacggg	aggcagcagc	aaggaatctt	gggcaatggg	cgaaagcctg	acccagcaac	360
gccgcgtgag	ggatgaaggc	tttcgggttg	taaacctctt	ttcacaggga	agaataatga	420
cgttacctgt	ggaataagct	tcggctaact	acgtgccagc	agccgcggtg	atacgtagga	480
agcaagcgtt	atccggattt	attgggcgta	aagttagcgt	aggtggtctt	tcaagttgga	540
tgtgaaattt	cccggcttaa	ccgggacgag	tcattcaata	ctggttgact	agagtacagc	600
aggagaaaac	ggaattcccg	gtgtagtgg	aaaatgcgta	gatatcggga	ggaacaccag	660
aggcgaaggc	ggttttctag	gttgtcactg	acactgaggc	tcgaaagcgt	ggggagcgaa	720
cagaattaga	tactctggtg	gtccacgcct	taaactatgg	acactaggtg	tagggagtat	780

cgaccctctc	tgtgccgaag	ctaacgcttt	aagtgtccc	cctggggagt	acggtcgcaa	840
ggctaaaact	caaaggaatt	gacgggggccc	cgcacaagca	gcgagagcgtg	tggtttaatt	900
cgatgctaca	cgaagaacct	taccaagatt	tgacatgcat	gaagtagtga	accgaaaggg	960
aaacgacctg	ttaagtcagg	agtttgacac	ggtgctgcat	ggctgtcgtc	agctcgtgcc	1020
gtgaggtgtt	tggtttaagtc	ctgcaacgag	cgcaaccctt	gttgctagtt	aaattttcta	1080
gcgagactgc	cccgcgaaac	ggggaggaag	gtggggatga	cgtcaagtca	gcatggcctt	1140
tatatcttgg	gctacacaca	cgctacaatg	gacagaacaa	taggttgcaa	cagtgtgaac	1200
tggagctaatt	cc					1212

<210> 6

<211> 1212

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 6

gatgaacgct	agcggcgtgc	cttatgcatg	caagtcgaac	ggtcttaagc	aattaagata	60
gtggcaaacg	ggtgagtaac	gcgtaagtaa	cctacctcta	agtgggggat	agcttcggga	120
aactgaaggt	aataccgcat	gtggtgggccc	gacataagtt	ggttcactaa	agccgtaagg	180
tgcttggtga	ggggcttgccg	tccgattagc	tagttggtgg	ggtaacggcc	taccaaggct	240
tcgatcggta	gctggtctga	gaggatgatc	agccacactg	ggactgagac	acggcccaga	300
ctcctacggg	aggcagcagc	aaggaatctt	gggcaatggg	cgaaagcctg	acccagcaac	360
gccgcgtgag	ggatgaaggc	tctcgggttg	ttaacctctt	ttcacaggga	agaataatga	420
cggtaacctgt	ggaataagct	tcggctaact	acgtgccagc	agccgcggta	atacgtagga	480
agcaagcgtt	atccggattt	attgggcgta	aagtgagcgt	aggtggtctt	tcaagttgga	540
tgtgaaaattt	cccggcttaa	ccgggacgtg	tcattcaata	ctggtggact	agagtacagc	600
aggagaaaac	ggaattccccg	gtgtagtggg	aaaatgcgta	gatatcggga	ggaacaccag	660
aggcgaaggc	ggttttctag	gttgtcactg	acactgaggc	tcgaaagcgt	ggggagcgaa	720
cagaattaga	tactctggta	gtccacgcct	taaactatgg	acactaggta	tagggagtat	780
cgaccctctc	tgtgccgaag	ctaacgcttt	aagtgtccc	cctggggagt	acggtcgcaa	840
ggctaaaact	caaaggaatt	gacgggggccc	cgcacaagca	gcgagagcgtg	tggtttaatt	900
cgatgctaca	cgaagaacct	taccaagatt	tgacatgcat	gaagtagtga	accgaaaggg	960
aaacgacctg	ttaagtcagg	agtttgacac	ggtgctgcat	ggctgtcgtc	agctcgtgcc	1020
gtgaggtgtt	tggtttaagtc	ctgcaacgag	cgcaaccctt	gttgctagtt	aaattttcta	1080
gcgagactgc	cccgcgaaac	ggggaggaag	gtggggatga	cgtcaagtca	gcatggcctt	1140
tatatcttgg	gctacacaca	cgctacaatg	gacagaacaa	taggttgcaa	cagtgtgaac	1200
tggagctaatt	cc					1212

<210> 7

<211> 1443

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 7

gatgaacgct	agcggcgtgc	cttatgcatg	caagtcgaac	ggtcttaagc	aattaagata	60
gtggcaaacg	ggtgagtaac	gcgtaagtaa	cctacctcta	agtgggggat	agcttcggga	120
aactgaaggt	aataccgcat	gtgatgggct	gacataagtc	ggttcattaa	agccgcaagg	180
tgcttggtga	ggggcttgccg	tccgattagc	tagttggtgg	ggtaatggtc	taccaaggct	240
tcgatcggta	gctggtctga	gaggatgatc	agccacactg	ggactgagac	acgggccaga	300
ctcctacggg	aggcagcagc	aaggaatctt	gggcaatggg	cgaaagcctg	acccagcaac	360
gccgcgtgag	ggatgaaggc	tttcgggttg	ttaacctctt	ttcacaggga	agaataatga	420
cggtaacctgt	ggaataagct	tcggctaact	acgtgccagc	agccgcggta	atacgtaggg	480
aagcaagcgt	tatccggatt	tattgggcgt	aaagtgagcg	taggtggtct	ttcaagtgg	540
atgtgaaatt	tcccggctta	accgggacgt	gtcattcaat	actggtggac	tagagtacag	600
caggagaaaa	cggaattccc	ggtgtagtgg	taaaatgcgt	agatatcggg	aggaaacacca	660
gaggcgaagg	cggttttcta	ggttgtcact	gacactgagg	ctcgaaagcg	tggggagcga	720
acagaattag	atactctggt	agtccacgcg	ttaactatg	gacactaggt	ataggagata	780
tcgaccctct	ctgtgccgaa	gtaaacgctt	ttaagtgtccc	gcctggggag	tacggtcgca	840
aggctaaaac	tcaaagggaat	tgacgggggc	ccgcaacaagc	agcggagcgt	gtggtttaatt	900
tcgatgctac	acgaagaact	taccaagatt	tgacatgcat	gaagtagtga	accgaaaggg	960
aaacgacctg	ttaagtcagg	agtttgacac	ggtgctgcat	ggctgtcgtc	agctcgtgcc	1020
gtgaggtgtt	gggttaagtc	ctgcaacgag	cgcaaccctg	ttgctagtta	aatTTTTctag	1080
cgagactgac	gagactgccc	cgcgaaacg	ggaggaaggt	ggggatgacg	tcaagtcagc	1140
atggccttta	tatcttgggc	tacacacag	ctacaatgga	cagaacaata	ggttgcaaca	1200
gtgtgaactg	gagctaattcc	ccaaagctgt	cctcagttcg	gattgcaggc	tgaacccgc	1260
ctgcatgaag	ttggagttgc	tagtaaccgc	atatcagcaa	ggtgcggtga	atacgttctc	1320
gggccttgta	cacaccgccc	gtcacgtcat	ganagccggt	aacacttgaa	gtcgtatgtgc	1380

caaccgcaag gaggcagtcg ccgaggggtgg gactggtaat tgggacgaag tcgtaacaag 1440
gta 1443

<210> 8
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CONSENSUS

<220>
<221> unsure
<222> (5)
<223> R=A/G

<220>
<221> unsure
<222> (11)
<223> Y=C/T

<220>
<221> unsure
<222> (18)
<223> W=A/T

<220>
<221> unsure
<222> (21)
<223> Y=C/T

<220>
<221> unsure
<222> (28)
<223> Y=T/C

<220>
<221> unsure
<222> (37)
<223> Y=T/C

<220>
<221> unsure
<222> (42)
<223> Y=C/T

<400> 8
tgtgrtgggc ygacatawgt yggttcayta aagccgyaag gygcttg 47

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 9
aagtcgaacg gtcttaagca 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 10
cgtcattatt cttccctgtg 20

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 11
gggaaacgac ctgttaagtc a 21

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 12
ggattagctc cagttcacac tg 22

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 13
aaatttaact agcaacaagg 20

<210> 14
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 14
ggagtatcga ccctctctg 19

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 15
gggagtatcg accctctc 18

<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 16
 agtgaaccga aagggaaa 18

 <210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 17
 gggttgtaaa cctcttttca c 21

 <210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 18
 gttagcttcg gcacagagag 20

 <210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 19
 tcagtgacaa cctagaaaac 20

 <210> 20
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 20
 gatgaacgct agcggcg 17

 <210> 21
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 21
 gtgccttatg catgcaag 18

 <210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 22
aatagggtgc aacagtgtga a 21

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 23
aatggacaga acaatagggt gc 22

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 24
ggcacatcga cttcaagtgt t 21

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 25
ggcacatcga cttcaagtgt t 21

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 26
taaccgggac gngtcattca 20

<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 27
gagtacagca ggagaaaac 19

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 28
 cctccttgcg gttggcacat c 21

 <210> 29
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PRIMER

 <400> 29
 ggcagtctcg ctagaaaat 19

 <210> 30
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CONSENSUS

 <220>
 <221> unsure
 <222> (3)
 <223> W=A/T

 <220>
 <221> unsure
 <222> (14)
 <223> M=A/C

 <220>
 <221> unsure
 <222> (22)
 <223> R=A/G

 <220>
 <221> unsure
 <222> (43)
 <223> R=A/G

 <220>
 <221> unsure
 <222> (44)
 <223> M=A/C

 <400> 30
 tgwagtagtg aacmgaaagg graacgacct gttaagtcag garmttgcac a 51

 <210> 31
 <211> 18
 <212> DNA
 <213> Dehalococcoides ethenogenes

 <400> 31
 attttctacg cgagactg 18

 <210> 32
 <211> 27
 <212> DNA
 <213> Dehalococcoides ethenogenes

<400> 32
attttctacg cgagactagc gagactg

27

<210> 33
<211> 1542
<212> DNA
<213> E. COLI

<400> 33
aaattgaaga gtttgatcat ggctcagatt gaacgctggc ggcaggccta acacatgcaa 60
gtcgaacggt aacaggaaga agcttgcttc tttgctgacg agtggcggac gggtagtaaa 120
tgtctgggaa actgcctgat ggagggggat aactactgga aacggtagct aataccgcat 180
aacgtcgcaa gaccaaagag ggggaccttc gggcctcttg ccatcggatg tgcccagatg 240
ggattagcta gtaggtgggg taacggctca cctaggcgac gatccctagc tggctctgaga 300
ggatgaccag ccacactgga actgagacac ggtccagact cctacgggag gcagcagtgg 360
ggaatattgc acaatgggag caagcctgat gcagccatgc cgcgtgtatg aagaaggcct 420
tcgggttgta aagtactttc agcggggagg aagggaagtaa agttaatacc tttgctcatt 480
gacgttacct gcagaagaag caccggctaa ctccgtgcca gcagccgcgg taatacggag 540
ggtgcaagcg ttaatcggaa ttactgggag taaagcgcac gcaggcgggt tgttaagtca 600
gatgtgaaat ccccgggctc aacctgggaa ctgcatctga tactggcaag cttgagcttc 660
gtagaggggg gtagaattcc aggtgtagcg gtgaaatgag tagagatctg gaggaatacc 720
ggtggcgaag gcggcccccgt ggacgaagac tgacgctcag gtgcgaaagc gtggggagca 780
aacaggatta gataccctgg tagtccacgc cgtaaacgat gtcgacttgg aggttgtgcc 840
cttgaggcgt ggcttcggga gctaacgcgt taagtgcacc gcctggggag tacggccgca 900
aggttaaaac tcaaataaat tgacgggggc ccgcacaagc ggtggagcat gtggtttaat 960
tcgatgcaac gcgaagaacc ttacctggct ttgacatcca cggaagtttt cagagatgag 1020
aatgtgcctt cgggaaccgt gagacagggt ctgcatggct gtcgtcagct cgtgttgtga 1080
aatgttgggt taagtccgcg aacgagcgca acccttatcc tttgttgcca gcggtccggc 1140
cgggaactca aaggagactg ccagtataaa actggaggaa ggtggggatg acgtcaagtc 1200
atcatggccc ttacgaccag ggctacacac gtgctacaat ggcgcataca aagagaagcg 1260
acctcgcgag agcaagcgga cctcataaag tgcgtcgtag tccggatttg agtctgcaac 1320
tcgactccat gaagtcgga tcgctagtaa tcgtggatca gaatgccacg gtgaatacgt 1380
tcccgggcct tgtacacacc gcccgtcaca ccatgggagt gggttgcaaa agaagtaggt 1440
agcttaacct tcgggagggc gcttaccact ttgtgattca tgactggggg gaagtcgtaa 1500
caaggttaacc gtaggggaac ctgcggttgg atcacctcct ta 1542

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
26 October 2000 (26.10.2000)

PCT

(10) International Publication Number
WO 00/63443 A3

- (51) International Patent Classification⁷: C12Q 1/68, 19707 (US). **EBERSOLE, Richard, C.** [US/US]; 2412 Dacia Drive, Wilmington, DE 19810 (US).
A62D 3/00
- (21) International Application Number: PCT/US00/09883 (74) Agent: **FELTHAM, S., Neil:** E.I. du Pont de Nemours and Company, Legal Patent Records Center, 1007 Market Street, Wilmington, DE 19898 (US).
- (22) International Filing Date: 13 April 2000 (13.04.2000)
- (25) Filing Language: English (81) Designated States (*national*): CA, MX, US.
- (26) Publication Language: English (84) Designated States (*regional*): European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).
- (30) Priority Data: 60/129,511 15 April 1999 (15.04.1999) US **Published:**
— with international search report
- (71) Applicant (*for all designated States except US*): **E.I. DU PONT DE NEMOURS AND COMPANY** [US/US]; 1007 Market Street, Wilmington, DE 19898 (US). (88) Date of publication of the international search report: 10 May 2002
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **HENDRICKSON, Edwin, R.** [US/US]; 49 Kings Grant Road, Hockessin, DE

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING BACTERIA

(57) Abstract: A unique 16S rRNA profile derived from *Dehalococcoides ethenogenes* has been identified and isolated. The profile contains a nucleic acid fragment that is linked to dechlorinating activity. This sequence is set forth in SEQ ID NO:1.

WO 00/63443 A3

INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 00/09883

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68 A62D3/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q A62D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, CHEM ABS Data, EMBASE, MEDLINE, BIOSIS, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MAYMO-GATELL XAVIER ET AL: "Isolation of a bacterium that reductively dechlorinates tetrachloroethene to ethene." SCIENCE (WASHINGTON D C), vol. 276, no. 5318, 1997, pages 1568-1571, XP002179676 ISSN: 0036-8075 the whole document & DATABASE EMBL:DEAF4928 'Online! EMBL; 4 July 1997 (1997-07-04) MAYMO-GATELL XAVIER ET AL: retrieved from EMBL, accession no. AF004928 Database accession no. EMBL:DEAF4928 abstract --- -/--	1-9

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

A document defining the general state of the art which is not considered to be of particular relevance

E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

Date of the actual completion of the international search

10 October 2001

Date of mailing of the international search report

23/10/2001

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Gabriels, J

INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 00/09883

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>HOLOMAN TRACEY R PULLIAM ET AL: "Characterization of a defined 2,3,5,6-tetrachlorobiphenyl-ortho-dechl orinating microbial community by comparative sequence analysis of genes coding for 16S rRNA." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 64, no. 9, 1998, pages 3359-3367, XP002179677 ISSN: 0099-2240 page 3364 -page 3366, left-hand column; table 2</p> <p>---</p>	1-9
X	<p>VON WINTZINGERODE FRIEDRICH ET AL: "Phylogenetic analysis of an anaerobic, trichlorobenzene-transforming microbial consortium." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 65, no. 1, January 1999 (1999-01), pages 283-286, XP002179679 ISSN: 0099-2240 page 284, right-hand column -page 286, left-hand column</p> <p>---</p>	1-9
X	<p>LAMONTAGNE M G ET AL: "Identification and analysis of PCB dechlorinating anaerobic enrichments by amplification: Accuracy of community structure based on restriction analysis and partial sequencing of 16S rRNA genes." JOURNAL OF APPLIED MICROBIOLOGY, vol. 84, no. 6, June 1998 (1998-06), pages 1156-1162, XP001024984 ISSN: 1364-5072 page 1157, right-hand column -page 1161, right-hand column</p> <p>---</p>	1-9
X	<p>FR 2 733 754 A (UNIV ANGERS) 8 November 1996 (1996-11-08) SEQ 3 of FR2733754 hybridises specifically with SEQ ID NO:2 of the oresent application example 1</p> <p>---</p>	1,3
X	<p>WO 98 49106 A (UNIV IOWA RES FOUND ;PARKIN GENE F (US); ALVAREZ PEDRO J (US); TIL) 5 November 1998 (1998-11-05)</p>	8,9
A	claims 1-3,42-45	1-9
A	<p>EP 0 864 542 A (SOLVAY DEUTSCHLAND) 16 September 1998 (1998-09-16) example 5</p> <p>---</p> <p>--- -/--</p>	1-9

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/09883

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>US 5 540 838 A (SMULLEN LYNN A ET AL) 30 July 1996 (1996-07-30) claim 1</p> <p>-----</p>	1-9

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/09883

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
FR 2733754	A	08-11-1996	FR 2733754 A1	08-11-1996
WO 9849106	A	05-11-1998	AU 7152298 A WO 9849106 A1	24-11-1998 05-11-1998
EP 0864542	A	16-09-1998	DE 19710010 A1 EP 0864542 A2	17-09-1998 16-09-1998
US 5540838	A	30-07-1996	NONE	